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| (54) Title: POLYNUCLEOTIDE POPULATION ISOLATED FROM NON-METASTATIC AND METASTATIC BREAST TUMOR TISSUES | | | | | | | | | | | | | | | | | | | | | |

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5 **POLYNUCLEOTIDE POPULATION ISOLATED FROM NON-
METASTATIC AND METASTATIC BREAST TUMOR TISSUES**

CROSS-REFERENCE TO RELATED APPLICATIONS

10 This application claims priority under 35 U.S.C. § 119(e) to the following U.S. Provisional Application Nos.: 60/090,039; 60/090,040; 60/090,041; 60/089,853; and 60/089,997, each filed June 19, 1998, the contents of which are hereby incorporated by reference into the present disclosure.

15 TECHNICAL FIELD

 This invention is in the field of genetic analysis. Specifically, the invention relates to the isolation of polynucleotides that are differentially expressed in primary or metastatic breast cancer. The compositions and methods of the present invention are particularly useful in diagnoses,
20 prognoses and/or treatment of breast cancer.

BACKGROUND OF THE INVENTION

 In spite of numerous advances in medical research, cancer remains the second leading cause of death in the United States. In the industrialized
25 nations, roughly one in five persons will die of cancer. Traditional modes of clinical care, such as surgical resection, radiotherapy and chemotherapy, have a significant failure rate, especially for solid tumors. Failure occurs either because the initial tumor is unresponsive, or because of recurrence due to regrowth at the original site and/or metastases.

30 Breast cancer is one of the most common cancers and is the third leading cause of death from cancers in the United States with an annual incidence of about 180,200 new cases among women in the United States

during 1997. About 1,400 new cases of breast cancer will be diagnosed in men in 1997. In industrialized nations, approximately one in eight women can expect to develop breast cancer. The overall mortality rate for breast cancer has remained unchanged since 1930. It has increased an average of 0.2% per year, but decreased in women under 65 years of age by an average of 0.3% per year. Preliminary data suggest that breast cancer mortality may be beginning to decrease, probably as a result of increased diagnoses of localized cancer and carcinoma *in situ*. See e.g., Marchant (1994) *Contemporary Management of Breast Disease II: Breast Cancer*, in: *Obstetrics and Gynecology Clinics of North America* 21:555-560; and Colditz (1993) *Cancer Suppl.* 71:1480-1489. An estimated 44,190 deaths (43,900 women, 290 men) in 1997 will occur due to breast cancer. The five-year survival rate for localized breast cancer has increased from 72% in the 1940s to 97% today. If the cancer has spread regionally, however, the rate is 76%, and for women with distant metastases the rate is 20%. Survival after a diagnosis of breast cancer continues to decline beyond five years. Sixty-five percent of women diagnosed with breast cancer survive 10 years and 56% survive 15 years.

Thus, despite an ongoing improvement in our understanding of the disease, breast cancer has remained resistant to medical intervention. Most clinical initiatives are focused on early diagnosis, followed by conventional forms of intervention, particularly surgery and chemotherapy. Such interventions are of limited success, particularly in patients where the tumor has undergone metastasis. There remains a considerable need in the art for developing diagnostic methods to monitor or prognose the progression of the disease. There also exists a pressing need to improve the arsenal of therapies available to provide more precise and more effective treatment in a less invasive way.

Tumor formation is a multi-step process where aberrant cells progressively accrue genetic mutations that confer a growth advantage or survival benefit. For example, cancer cells from metastatic lesions have been found to be more aggressive with respect to their rate of growth and capacity to invade other tissues as compared to cancer cells derived from primary

tumors. It is known that genotypic alterations contribute to the aggressive phenotype of metastatic tumor cells. Due to the vast variability in the nature of the genotypic alterations, the identification of genes preferentially expressed in either non-metastatic breast tumor cells or metastatic breast cells has been difficult. Undoubtly, an exhausted search for such genes have considerable value in both the diagnosis of breast cancer as well as in devising new therapeutic strategies to combat this disease.

DISCLOSURE OF THE INVENTION

The present invention addresses these and certain other deficiencies in the prior art in having isolated and characterized a population of polynucleotides corresponding to genes or transcripts that are differentially expressed or transcribed in either non-metastatic or metastatic breast tumor cells. Transcripts that are overexpressed in the non-metastatic breast tumor such as a primary tumor may encode factors that restrict tumor cell growth such as tumor suppressors, pro-apoptotic factors, inhibitory growth factors or molecules that engage in immune recognition. Transcripts that are preferentially expressed in metastatic tumor tissue may encode factors that augment tumor cell growth or confer a survival benefit such as oncogenes, stimulatory growth factors, anti-apoptotic factors or immunosuppressive factors. These populations of polynucleotides associated with the non-metastatic or metastatic state of a breast cell are particularly useful in the diagnoses and the development of therapeutics for metastatic breast cancer.

Accordingly, the present invention provides a method for aiding in the diagnoses of the metastatic condition of a breast cell by determining differential expression of a polynucleotide that is associated with breast cancer progression. In one aspect, the differential expression is characterized by over expression of a polynucleotide having the sequence selected from the group set forth in Table 1, or the encoded polypeptide. In another aspect, the differential expression is characterized by under-expression of a polynucleotide having the sequence selected from the group set forth in Table 2, or the encoded polypeptide.

Another embodiment of the invention is a screen for a potential therapeutic agent that modulates the expression of a polynucleotide associated with the metastatic condition of a breast tumor cell. The method involves contacting a cell with an effective amount of a potential agent, and assaying
5 for a change in expression level of a polynucleotide selected from the group identified in Tables 1 and 2, wherein a change in the expression level is indicative of a candidate therapeutic agent. The potential therapeutic agent can be, but is not limited to, an antisense oligonucleotide, a ribozyme, a ribozyme derivative, an antibody, a liposome, a small molecule, or an inorganic
10 compound.

Yet another embodiment of the invention is a method of reversing the metastatic condition of a breast cell, wherein the cell is characterized by differential expression of polynucleotides of the invention. In the method, a cell is contacted with an agent identified by the above-mentioned method.
15 Still yet another embodiment of the invention is a method of modulating the genotype and/or phenotype of a breast cell by introducing the cell a polynucleotide of the present invention. In one embodiment a polynucleotide or regulatory sequence identified to inhibit the metastatic potential of the tumor cell is introduced into the cell.

20 The present invention also provides isolated polynucleotides and populations of the isolated polynucleotides that identify a non-metastatic or a metastatic breast tumor cell. The polynucleotides are intended to include DNA, cDNA, RNA and genomic DNA. Expression systems, including gene delivery vehicles such as liposomes, plasmids and viral vectors, and host cells
25 containing the polynucleotides are further provided by this invention.

Further provided are promoter sequences derived from the tags represented in either of Tables 1 or 2.

Additionally, the invention includes nucleic acid probes and primers that hybridize to invention polynucleotides, as well as isolated nucleic acids
30 comprising novel, expressed gene sequences containing these polynucleotides. The present invention also provides polypeptides and proteins encoded by the polynucleotides.

The present invention further provides antisense oligonucleotides, antibodies, hybridoma cell lines and compositions containing the same.

Further provided are polynucleotides that correspond to regulatory sequence to enhance or inhibit of downstream polynucleotides. The regulatory
5 sequences can be inserted upstream of polynucleotides encoding therapeutic genes.

Also provided are databases of sequences cataloging polynucleotides differentially expressed in non-metastatic or metastatic breast cells and methods of using the sequences to identify and analyze genes expressed in a
10 test cell. In one aspect, the sequences are downregulated in a metastatic breast cell and comprises at least one polynucleotide selected from the group identified in Table 2, and their respective complements in a computer readable form. In another aspect, the database of sequences characterizes a metastatic breast cell and contains at least one polynucleotide selected from the group
15 identified in Table 1, and their respective complements in a computer readable form.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

Sequence ID Numbers 1 through 3175 depict the tags corresponding to
20 distinct transcripts that are preferentially transcribed in the metastatic breast tumor tissue.

Sequence ID Numbers 3176 through 5911 depict the tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumor tissue.

25

MODE(S) FOR CARRYING OUT THE INVENTION

Throughout this disclosure, various publications, patents and published patent specifications are referenced by an identifying citation. The disclosures of these publications, patents and published patent specifications are hereby
30 incorporated by reference into the present disclosure to more fully describe the state of the art to which this invention pertains.

Definitions

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of immunology, molecular biology, microbiology, cell biology and recombinant DNA. These methods are described in the following publications. See, *e.g.*, Sambrook et al., MOLECULAR CLONING: A LABORATORY MANUAL, 2nd edition (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (F. M. Ausubel, et al. eds., (1987)); the series METHODS IN ENZYMOLOGY (Academic Press, Inc.); "PCR: A PRACTICAL APPROACH" (M. MacPherson et al., IRL Press at Oxford University Press (1991)); PCR 2: A PRACTICAL APPROACH (M.J. MacPherson, B.D. Hames and G.R. Taylor eds. (1995)); ANTIBODIES, A LABORATORY MANUAL (Harlow and Lane, eds. (1988)); and ANIMAL CELL CULTURE (R.I. Freshney, ed. (1987)).

As used in the specification and claims, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a cell" includes a plurality of cells, including mixtures thereof.

The term "comprising" is intended to mean that the compositions and methods include the recited elements, but not excluding others. "Consisting essentially of" when used to define compositions and methods, shall mean excluding other elements of any essential significance to the combination. Thus, a composition consisting essentially of the elements as defined herein would not exclude trace contaminants from the isolation and purification method and pharmaceutically acceptable carriers, such as phosphate buffered saline, preservatives, and the like. "Consisting of" shall mean excluding more than trace elements of other ingredients and substantial method steps for administering the compositions of this invention. Embodiments defined by each of these transition terms are within the scope of this invention.

The terms "polynucleotide" and "oligonucleotide" can be used interchangeably, and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof.

Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant
5 polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The
10 sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

The polynucleotides can be both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of the
15 invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

A "gene" refers to a polynucleotide containing at least one open reading frame that is capable of encoding a particular protein after being
20 transcribed and translated.

A "gene product" refers to the amino acid (e.g., peptide or polypeptide) generated when a gene is transcribed and translated.

As used herein a second polynucleotide "corresponds to" another (a first) polynucleotide if it is related to the first polynucleotide by any of the
25 following relationships:

- 1) The second polynucleotide comprises the first polynucleotide and the second polynucleotide encodes a gene product.
- 2) The second polynucleotide is 5' or 3' to the first polynucleotide in cDNA, RNA, genomic DNA, or fragment of any of these
30 polynucleotides. For example, a second polynucleotide may be a fragment of a gene that includes the first and second polynucleotides. The first and second polynucleotides are related in

that they are components of the gene coding for a gene product, such as a protein or antibody. However, it is not necessary that the second polynucleotide comprises or overlaps with the first polynucleotide to be encompassed within the definition of “corresponding to” as used herein. For example, the first polynucleotide may be a fragment of a 3’ untranslated region of the second polynucleotide, for example a promoter sequence. The first and second polynucleotide may be fragment of a gene coding for a gene product. The second polynucleotide may be an exon of the gene while the first polynucleotide may be an intron of the gene.

3) The second polynucleotide is the complement of the first polynucleotide.

The “genotype” of a cell refers to the genetic makeup of the cell and/or its gene expression profile. Modulation of the genotype of a cell can be achieved by introducing additional DNA or RNA either as episomes or as an integral part of the chromosomal DNA of the recipient cell. The genotype can also be modulated by altering the expression level, e.g. mRNA abundance, of a particular gene using agents that regulate gene expression.

A “sequence tag” or “tag” or “SAGE tag” is a short sequence, generally under about 20 nucleotides, that occurs in a certain position in messenger RNA. The tag can be used to identify the corresponding transcript and gene from which it was transcribed. A “ditag” is a dimer of two sequence tags.

A “database” denotes a set of stored data which represent a collection of sequences including nucleotide and peptide sequences, which in turn represent a collection of biological reference materials.

A “probe” is any biochemical labeled with radioactive isotopes or tagged in other ways for ease in identification. A probe is used to identify or isolate a gene, a gene product, or a protein. Examples of probes include, but are not limited to, a radioactive mRNA hybridizing with a single strand of its DNA gene, a DNA or cDNA hybridizing with its complementary region in a chromosome, or a monoclonal antibody combining with a specific protein.

A "promoter" is a region on a DNA molecule to which an RNA polymerase binds and initiates transcription. In an operon, the promoter is usually located at the operator end, adjacent but external to the operator. The nucleotide sequence of the promoter determines both the nature of the enzyme that attaches to it and the rate of RNA synthesis.

A "primer" is a short polynucleotide, generally with a free 3' -OH group, that binds to a target or "template" potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target.

The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation, such as conjugation with a labeling component. As used herein the term "amino acid" refers to either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics.

As used herein, the term "isolated" means separated from constituents, cellular and otherwise, in which the polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, are normally associated with in nature. As is apparent to those of skill in the art, a non-naturally occurring the polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, does not require "isolation" to distinguish it from its naturally occurring counterpart. In one embodiment, an "isolated" polynucleotide is separated from the 5' and 3' non-coding but contiguous sequences with which it is normally associated with in nature. In addition, a "concentrated", "separated" or "diluted" polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, is distinguishable from its naturally occurring counterpart in that the concentration or number of molecules per volume is greater than "concentrated" or less than "separated" than that of its naturally occurring

counterpart. A polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, which differs from the naturally occurring counterpart in its primary sequence or for example, by its glycosylation pattern, need not be present in its isolated form since it is distinguishable from its naturally occurring counterpart by its primary sequence, or alternatively, by another characteristic such as glycosylation pattern. Thus, a non-naturally occurring polynucleotide is provided as a separate embodiment from the isolated naturally occurring polynucleotide. A protein produced in a bacterial cell is provided as a separate embodiment from the naturally occurring protein isolated from a eucaryotic cell in which it is produced in nature.

As used herein, "expression" refers to the process by which polynucleotides are transcribed into mRNA and/or the process by which the transcribed mRNA (also referred to as "transcript") is subsequently being translated into peptides, polypeptides, or proteins. The transcripts and the encoded polypeptides are collectively referred to as gene product. If the polynucleotide is derived from genomic DNA, expression may include splicing of the mRNA in an eukaryotic cell.

"Differentially expressed" or "differential expression", as applied to nucleotide sequence or polypeptide sequence in a cell or a tissue, refers to overexpression or underexpression of that polynucleotide when compared to that expressed in a control cell or tissue. Underexpression also encompasses absence of expression of a particular polynucleotide as evidenced by the absence of detectable expression in a tested sample when compared to a control. The selection of the appropriate control cell or tissue is dependent on the sample cell or tissue initially selected and the phenotype of the sample that is under investigation. For instance, if the sample cell is a non-metastatic cell derived from a primary tumor, one or more counterparts or metastatic cells of the sample cell can be used as control cells. Counterparts would include, for example, cell lines established from the same or related cells to those found in the sample cell population. For example, the control cell can be any of a counterpart benign cell type, a counterpart non-metastatic cell type.

A gene or transcript is associated with "breast cancer progression" if it yields transcription or translation products at a substantially altered level or in a substantially altered form in cells derived from metastatic breast tumor tissues as compared with cells of a control tissue, and which may play a role in breast
5 tumor metastasis. The gene or transcript can be a normally quiescent gene that becomes activated (such as a dominant cancer-causing gene); it may be a gene that becomes expressed at an abnormally high level; it may be a gene that becomes mutated to produce a variant phenotype; it may be a gene that becomes expressed at an abnormally low level (such as a cancer suppresser gene); or it
10 may be a gene exhibiting differential expression, in which the differential expression correlates with tumor metastasis.

A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made of a target polynucleotide using a "pair of primers" or a "set of primers" consisting of an "upstream" and a "downstream" primer, and a
15 catalyst of polymerization, such as a DNA polymerase, and typically a thermally-stable polymerase enzyme. Methods for PCR are well known in the art, and taught, for example in MacPherson et al., (1991) and (1995), *supra*. All processes of producing replicate copies of a polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "replication." A primer
20 can also be used as a probe in hybridization reactions, such as Southern or Northern blot analyses.

"Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding
25 may occur by Watson-Crick base pairing, Hoogsteen binding, or in any other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the
30 initiation of a PCR reaction, or the enzymatic cleavage of a polynucleotide by a ribozyme.

Hybridization reactions can be performed under conditions of different “stringency”. In general, a low stringency hybridization reaction is carried out at about 40 °C in 10 X SSC or a solution of equivalent ionic strength/temperature. A moderate stringency hybridization is typically performed at about 50 °C in 6 X SSC, and a high stringency hybridization reaction is generally performed at about 60 °C in 1 X SSC.

When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, the reaction is called “annealing” and those polynucleotides are described as “complementary”. A double-stranded polynucleotide can be “complementary” or “homologous” to another polynucleotide, if hybridization can occur between one of the strands of the first polynucleotide and the second. “Complementarity” or “homology” (the degree that one polynucleotide is complementary with another) is quantifiable in terms of the proportion of bases in opposing strands that are expected to form hydrogen bonding with each other, according to generally accepted base-pairing rules. A polynucleotide that is 100% complementary to a second polynucleotide is understood to be “complements” of each other.

“Tumor” or “cancer” comprises a localized population of proliferating cells in an animal that are not governed by the usual limitation of normal growth. The tumor is said to be benign if it does not undergo metastasis and malignant if it undergoes metastasis. A metastatic cell or tissue means that the cell can invade and destroy neighboring body structures.

A “composition” is intended to mean a combination of active agent and another compound or composition, inert (for example, a detectable agent or label) or active, such as an adjuvant.

A “pharmaceutical composition” is intended to include the combination of an active agent with a carrier, inert or active, making the composition suitable for diagnostic or therapeutic use *in vitro*, *in vivo* or *ex vivo*.

As used herein, the term “pharmaceutically acceptable carrier” encompasses any of the standard pharmaceutical carriers, such as a phosphate

buffered saline solution, water, and emulsions, such as an oil/water or water/oil emulsion, and various types of wetting agents. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers and adjuvants, see Martin, REMINGTON'S PHARM. SCI., 15th Ed. (Mack Publ. Co., Easton (1975)).

An "effective amount" is an amount sufficient to effect beneficial or desired results. An effective amount can be administered in one or more administrations, applications or dosages.

A "subject," "individual" or "patient" is used interchangeably herein, which refers to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, simians, humans, farm animals, sport animals, and pets.

A "control" is an alternative subject or sample used in an experiment for comparison purpose. A control can be "positive" or "negative". For example, where the purpose of the experiment is to determine a correlation of an altered expression level of a gene with a particular type of cancer, it is generally preferable to use a positive control (a subject or a sample from a subject, carrying such alteration and exhibiting syndromes characteristic of that disease), and a negative control (a subject or a sample from a subject lacking the altered expression and clinical syndrome of that disease).

A "gene delivery vehicle" is defined as any molecule that can carry inserted polynucleotides into a host cell. Examples of gene delivery vehicles are liposomes, viruses, such as baculovirus, adenovirus and retrovirus, bacteriophage, cosmid, plasmid, fungal vectors and other recombination vehicles typically used in the art which have been described for expression in a variety of eukaryotic and prokaryotic hosts, and may be used for gene therapy as well as for simple protein expression.

A "viral vector" is defined as a recombinantly produced virus or viral particle that comprises a polynucleotide to be delivered into a host cell, either *in vivo*, *ex vivo* or *in vitro*. Examples of viral vectors include retroviral vectors, adenovirus vectors, adeno-associated virus vectors and the like. In aspects where gene transfer is mediated by a retroviral vector, a vector

construct refers to the polynucleotide comprising the retroviral genome or part thereof, and a therapeutic gene. As used herein, "retroviral mediated gene transfer" or "retroviral transduction" carries the same meaning and refers to the process by which a gene or nucleic acid sequences are stably transferred
5 into the host cell by virtue of the virus entering the cell and integrating its genome into the host cell genome. The virus can enter the host cell via its normal mechanism of infection or be modified such that it binds to a different host cell surface receptor or ligand to enter the cell. As used herein, retroviral vector refers to a viral particle capable of introducing exogenous nucleic acid
10 into a cell through a viral or viral-like entry mechanism.

Retroviruses carry their genetic information in the form of RNA; however, once the virus infects a cell, the RNA is reverse-transcribed into the DNA form which integrates into the genomic DNA of the infected cell. The integrated DNA form is called a provirus.

15 In aspects where gene transfer is mediated by a DNA viral vector, such as an adenovirus (Ad) or adeno-associated virus (AAV), a vector construct refers to the polynucleotide comprising the viral genome or part thereof, and a therapeutic gene. Adenoviruses (Ads) are a relatively well characterized, homogenous group of viruses, including over 50 serotypes (see, *e.g.*,
20 WO 95/27071). Ads are easy to grow and do not require integration into the host cell genome. Recombinant Ad-derived vectors, particularly those that reduce the potential for recombination and generation of wild-type virus, have also been constructed (see, WO 95/00655; WO 95/11984). Wild-type AAV has high infectivity and specificity integrating into the host cells genome.
25 (Hermonat and Muzyczka (1984) *PNAS USA* 81:6466-6470; Lebkowski et al. (1988) *Mol. Cell. Biol.* 8:3988-3996).

Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA *in vitro* or *in vivo*, and are
30 commercially available from sources such as Stratagene (La Jolla, CA) and Promega Biotech (Madison, WI). In order to optimize expression and/or *in vitro* transcription, it may be necessary to remove, add or alter 5' and/or 3'

untranslated portions of the clones to eliminate extra, potential inappropriate alternative translation initiation codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5'
5 of the start codon to enhance expression.

Gene delivery vehicles also include several non-viral vectors, including DNA/liposome complexes, and targeted viral protein DNA complexes. Liposomes that also comprise a targeting antibody or fragment thereof can be used in the methods of this invention. To enhance delivery to a cell, the
10 nucleic acid or proteins of this invention can be conjugated to antibodies or binding fragments thereof which bind cell surface antigens, e.g., TCR, CD3 or CD4.

"Host cell" is intended to include any individual cell or cell culture which can be or have been recipients for vectors or the incorporation of
15 exogenous polynucleotides, polypeptides and/or proteins. It also is intended to include progeny of a single cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. The cells may be procaryotic or eucaryotic, and include but are not limited to
20 bacterial cells, yeast cells, plant cells, insect cells, animal cells, and mammalian cells, e.g., murine, rat, simian or human.

An "antibody" is an immunoglobulin molecule capable of binding an antigen. As used herein, the term encompasses not only intact immunoglobulin molecules, but also anti-idiotypic antibodies, mutants,
25 fragments, fusion proteins, humanized proteins and modifications of the immunoglobulin molecule that comprise an antigen recognition site of the required specificity. The specificity of an antibody refers to the ability of the antibody to distinguish polypeptides comprising the immunizing epitope from other polypeptides.

30 As used herein, "solid phase support" is not limited to a specific type of support. Rather a large number of supports are available and are known to one of ordinary skill in the art. Solid phase supports include silica gels, resins,

derivatized plastic films, glass beads, cotton, plastic beads, alumina gels. A suitable solid phase support may be selected on the basis of desired end use and suitability for various synthetic protocols. For example, for peptide synthesis, solid phase support may refer to resins such as polystyrene (*e.g.*,
5 PAM-resin obtained from Bachem Inc., Peninsula Laboratories, etc.), POLYHIPE® resin (obtained from Aminotech, Canada), polyamide resin (obtained from Peninsula Laboratories), polystyrene resin grafted with polyethylene glycol (TentaGel®, Rapp Polymere, Tübingen, Germany) or polydimethylacrylamide resin (obtained from Milligen/Bioscience, California).
10 In a preferred embodiment for peptide synthesis, solid phase support refers to polydimethylacrylamide resin.

The phenotype of a cell is determined by the genes expressed within it. The total of expressed genes can be identified by the “transcripts” (transcribed
15 genes represented by the mRNA population) present in the cell. The totality of transcripts present in any particular cell, affected by certain environmental factors or stimuli, and with varying levels of expression of various transcripts in the cell, can be represented by a “transcriptome”. The transcriptome is one means by which to identify the cell.

20 Serial Analysis of Gene Expression or “SAGE” (Velculescu, et al. (1995) *Science* 270:484-487 and U.S. Patent No. 5,695,937), provides the tool by which the expressed genes and the expression level of the genes of a cell at any one point in the cell cycle and under various environmental stimuli are isolated, sequenced and cataloged. SAGE provides quantitative gene
25 expression data without the prerequisite of a hybridization probe for each transcript. SAGE is based on two principles. First, a short sequence tag (9-11 base pairs) contains sufficient information to uniquely identify a transcript, provided that it is derived from a defined location within that transcript. Second, many transcript tags can be concatenated into a single
30 molecule and then sequenced, revealing the identity of multiple tags simultaneously. The expression pattern of any population of transcripts can be quantitatively evaluated by determining the abundance of individual tags and

identifying the gene corresponding to each tag. Velculescu et al. (1995) *supra* at 484.

Primary and metastatic breast tumor tissue from the same individual has been subjected to SAGE and the tags isolated from each population were compared and analyzed. Therapeutic relevant tags have been isolated. The polynucleotides comprising or corresponding to these tags, as well as polypeptides and antibodies thereto, are aspects of the present invention.

Polynucleotides, Vectors and Host Cells of the Invention

The present invention provides a polynucleotide and populations of polynucleotides that are differentially expressed in a non-metastatic breast tumor as compared to a metastatic breast tumor, or vice versa. The populations of polynucleotides are characterized in whole or in part by the tags represented in Tables 1 and 2, below, or their respective complements. A polynucleotide is determined to be differentially expressed in a non-metastatic breast tumor cell if it is "overexpressed" or "underexpressed" at least 3 fold higher or less the same or corresponding polynucleotide in the metastatic counterpart. In one embodiment, the population of polynucleotides contains tags corresponding to transcripts that are overexpressed in cells derived from a primary breast tumor. In another embodiment, the population of polynucleotides contains tags or transcripts that are overexpressed in cells derived from a metastatic breast tumor. In further embodiments, the transcript or gene has been previously characterized, but was heretofore unknown to be differentially expressed in a metastatic or a non-metastatic breast tumor tissue. These genes or transcripts can be identified, in whole or in part, by specifically hybridizing under moderate or stringent conditions to the polynucleotides comprising or corresponding to polynucleotides identified in Tables 1 and 2, or their respective complements, using the methods described below.

This invention also provides several embodiments comprising different populations identified by the Sequence ID Nos. as follows: 1, 1-5, 1-17, 18-24, Nos. 1-24, 25-36, 1-36, 18-36, 37-53, 54-74, 37-74, 1-53, 1-74, 75-116, 1-116, 117-279, 1-279, 280-549, 1-549, 550-1160, 1-1160, 1161-3175, 1-3175,

3176-3183, 3184-3197, 3176-3197, 3198-3204, 3176-3204, 3205-3213, 3176-3213, 3214-3226, 3176-3226, 3227-3242, 3176-3242, 3243-3294-3176-3294, 3295-3381, 3176-3381, 3382-3554, 3176-3354, 3555-4012, 3176-4012, 4013-5911-3176-5911, 1-5911, or any combination thereof.

- 5 In a separate embodiment, the genes or transcripts are identified using sequence homology or alignment software and sequence databases, as described below.

Hybridization can be performed under conditions of different “stringency”. Conditions that vary levels of stringency are well known in the art. See, for example, Sambrook, et al. *supra*. Briefly, relevant conditions include temperature, ionic strength, time of incubation, the presence of additional solutes in the reaction mixture such as formamide, and the washing procedure. Higher stringency conditions are those conditions, such as higher temperature and lower sodium ion concentration, which require higher minimum complementarity between hybridizing elements for a stable hybridization complex to form. In general, a moderate stringency hybridization is typically performed at about 50 °C in 6 X SSC, and a high stringency hybridization reaction is generally performed at about 60 °C in 1 X SSC.

- 20 A number of the polynucleotide sequences disclosed herein are “novel”, that is, the tag or its respective complement, lacks substantial sequence homology with any previously identified Expressed Sequence Tags (“EST”) or characterized gene sequences. The inventors have searched databases and if no match is found, the “Description” column is blank indicating that no tag has been identified. If the tag corresponds to an EST or gene, the accession number and/or description of the gene or its product are provided in the Tables.

- Additional sequence homology searches can be made with the aid of computer methods. A variety of software programs are available in the art. Non-limiting examples of these programs are Blast (Blast is available from the worldwide web at <http://www.ncbi.nlm.nih.gov/BLAST/>), DNA Star, MegAlign, and GeneJockey. Any sequence database that contains DNA or

protein sequences corresponding to a gene or a segment thereof can be used for sequence analysis. Commonly employed databases include but are not limited to GenBank, EMBL, DDBJ, PDB, SWISS-PROT, EST, STS, GSS, and HTGS. Sequence similarity can be discerned by aligning the tag sequence
5 against a DNA sequence database. Alternatively, the tag sequence can be translated into six reading frames; the predicted peptide sequences of all possible reading frames are then compared to individual sequences stored in a protein database. Parameters for determining the extent of homology set forth by one or more of the aforementioned alignment programs are well established
10 in the art. They include but are not limited to p value and percent sequence identity. P value is the probability that the alignment is produced by chance. For a single alignment, the p value can be calculated according to Karlin et al. (1990) *Proc. Natl. Acad. Sci* 87: 2246. For multiple alignments, the p value can be calculated using a heuristic approach such as the one programmed in
15 Blast. Percent sequence identify is defined by the ratio of the number of nucleotide or amino acid matches between the query sequence and the known sequence when the two are optimally aligned. A tag sequence is considered to lack substantial homology with any known sequences when the regions of alignment of comparable length exhibit less than 30% of sequence identity,
20 more preferably less than 20% identity, even more preferably less than 10% identity.

The polynucleotides embodied in the present invention also include larger fragments or the full length coding sequences that comprise a novel sequence identified in Tables 1 and 2. Based on the novel sequences disclosed
25 herein, fragments or the full length coding sequences of the corresponding novel transcripts or genes can be identified using various cloning methods known to artisans in the art. Five methods are disclosed in the section "Methods of Cloning Novel Transcripts or Genes" which further assist practitioners of ordinary skill to isolate these transcripts, genes or cDNA
30 containing or corresponding to the tag sequences of the invention.

In addition to the sequences shown in Tables 1 and 2, this invention also provides the anti-sense polynucleotide stand, e.g. antisense RNA to these

sequences or their complements. One can synthesize an antisense RNA based on the sequences provided in the Tables using any methods available in the art, such as the methodology described in Vander Krol et al. (1988) *BioTechniques* 6:958.

5 The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but encode substantially the same amino acid sequences. These altered, but phenotypically equivalent polynucleotides are referred to as "functionally equivalent nucleic acids." As used herein, "functionally equivalent nucleic acids" encompass nucleic acids
10 characterized by slight and non-consequential sequence variations that will function in substantially the same manner to produce the same protein product(s) as the nucleic acids disclosed herein (e.g. by virtue of the degeneracy of the genetic codes), or that have conservative amino acid variations. For example, conservative variations include substitution of a non-
15 polar residue with another non-polar residue, or substitution of a charged residue with a similarly charged residue. These sequence variations include those recognized by artisans in the art as those that do not substantially alter the tertiary structure of the encoded protein.

 The polynucleotides of the invention can comprise and can be used to
20 identify additional sequences, such as additional encoding sequences within the same transcription unit, controlling elements such as promoters, ribosome binding sites, and polyadenylation sites, additional transcription units under control of the same or a different promoter, sequences that permit cloning, expression, and transformation of a host cell, and any such construct as may be
25 desirable to provide embodiments of this invention.

 This invention also provides a promoter sequence derived from cell's genome, wherein the promoter sequence corresponds to the regulatory region of a gene that is differentially expressed in the cell as compared to a control cell. The promoters are identified and characterized by: 1) probing a cDNA
30 library with a probe corresponding to the SAGE tag sequence or generating a portion of the desired cDNA by conducting anchored PCR using primers based on the SAGE tag sequence. Examples of cell types wherein differential

expression of a gene is related to promoter function include using the partial cDNA product obtained in step one above as a probe, cloning the extreme 5' end of the cDNA, and also by using the 5' end of the cDNA as a probe, cloning from a genomic library the promoter of the gene that encodes the cDNA. These promoters are identified using the methods described below in combination with standard molecular techniques. Functionally equivalent sequences, as defined above, are further provided by this invention.

In one aspect, the promoter is a sequence derived from the genome of a metastatic cell's genome, wherein the promoter region corresponds to the regulatory region of a gene that is differentially expressed in the cell as compared to the non-metastatic cell. Alternatively, the promoter is a sequence derived from the genome of a non-metastatic cell's genome, wherein the promoter region corresponds to the regulatory region of a gene that is differentially expressed in the cell as compared to the metastatic cell. Table 1 and 2, below are examples of such a sort.

The promoters identified above can be operatively linked to a foreign polynucleotide to compel differential expression of the foreign polynucleotide. A foreign polynucleotide is intended to include any sequence which encodes in whole or in part a polypeptide or protein. It also includes sequences encoding ribozymes and antisense molecules.

Foreign polynucleotides also include therapeutic genes that encode dominant inhibitory oligonucleotides and peptides as well as genes that encode regulatory proteins and oligonucleotides. Generally, gene therapy will involve the transfer of a single therapeutic gene although more than one gene may be necessary for the treatment of particular diseases. In one embodiment, the therapeutic gene is a dominant inhibiting mutant of the wild-type immunosuppressive agent. Alternatively, the therapeutic gene could be a wild-type copy of a defective gene or a functional homolog.

In one aspect, a tag identified by any of Seq. ID Nos. 1 through 5911 corresponds to or comprises a polynucleotide that encodes a polypeptide or protein that is biologically active as an antigen, e.g., a native antigen, an altered antigen, a self-antigen or a tumor-associated antigen. Antigens are

identified by noting the overexpression or cell-specific expression of a tag identified herein. Using the methods described below, the gene comprising or corresponding to the tag is identified, cloned and inserted into an APC. The tag corresponds to an antigen if a CTL response is raised under appropriate experimental conditions. The peptide is confirmed immunogenic if an appropriate immune response is elicited.

The invention also encompasses co-administration of an immunostimulatory factor and a foreign polynucleotide, both under the control of promoters. In one embodiment, the promoter is an APC specific promoter. In alternative embodiment, the promoters are specific to tissue identified in Tables 1 and 2. The immunostimulatory factors of this invention include any polypeptide factors that modulate immune responses mediated by APC and corresponding T cells. For example, co-stimulatory factors that are differentially expressed in APCs can be used directly to boost the APC functions *in vivo*. Co-stimulatory factors have been described above.

The polynucleotides of the invention can be introduced and expressed in a suitable host cell for generating a cell-based vaccine. These methods are described in more detail below.

The polynucleotides can be conjugated to a detectable marker, e.g., an enzymatic label or a radioisotope for detection of nucleic acid and/or expression of the gene in a cell. A wide variety of appropriate detectable markers are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred embodiments, one will likely desire to employ a fluorescent label or an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary nucleic acid-containing samples.

The polynucleotides embodied in this invention can be obtained using chemical synthesis, recombinant cloning methods, PCR, or any combination

thereof. Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequence data provided herein to obtain a desired polynucleotide by employing a DNA synthesizer or ordering from a commercial service.

5 Polynucleotides comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides can be introduced into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct uptake, endocytosis, transfection, f-
10 mating or electroporation. Once introduced, the exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. Amplified DNA can be isolated from the host cell by standard methods. See, e.g., Sambrook, et al. (1989) *supra*. RNA can also be obtained from transformed host cell, or it can be obtained directly
15 from the DNA by using a DNA-dependent RNA polymerase.

The present invention further encompasses a variety of gene delivery vehicles comprising the polynucleotide of the present invention. Gene delivery vehicles include both viral and non-viral vectors such as naked plasmid DNA or DNA/liposome complexes. Vectors are generally categorized
20 into cloning and expression vectors. Cloning vectors are useful for obtaining replicate copies of the polynucleotides they contain, or as a means of storing the polynucleotides in a depository for future recovery. Expression vectors (and host cells containing these expression vectors) can be used to obtain polypeptides produced from the polynucleotides they contain. Suitable
25 cloning and expression vectors include any known in the art, e.g., those for use in bacterial, mammalian, yeast and insect expression systems. The polypeptides produced in the various expression systems are also within the scope of the invention and are described above.

When the vectors are used for gene therapy *in vivo* or *ex vivo*, a
30 pharmaceutically acceptable vector is preferred, such as a replication-incompetent retroviral or adenoviral vector. Pharmaceutically acceptable vectors containing the nucleic acids of this invention can be further modified

for transient or stable expression of the inserted polynucleotide. As used herein, the term "pharmaceutically acceptable vector" includes, but is not limited to, a vector or delivery vehicle having the ability to selectively target and introduce the nucleic acid into dividing cells. An example of such a
5 vector is a "replication-incompetent" vector defined by its inability to produce viral proteins, precluding spread of the vector in the infected host cell. An example of a replication-incompetent retroviral vector is LNL6 (Miller A.D. et al. (1989) *BioTechniques* 7:980-990). The methodology of using replication-incompetent retroviruses for retroviral-mediated gene transfer of gene markers
10 is well established (Correll et al. (1989) *PNAS USA* 86:8912; Bordignon (1989) *PNAS USA* 86:8912-52; Culver K. (1991) *PNAS USA* 88:3155; and Rill, D.R. (1991) *Blood* 79(10):2694. Clinical investigations have shown that there are few or no adverse effects associated with the viral vectors, see Anderson (1992) *Science* 256:808-13.

15 Compositions containing the polynucleotides of this invention, in isolated form or contained within a vector or host cell are further provided herein. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

A vector of this invention can contain one or more polynucleotides
20 comprising a sequence selected from SEQ ID NOS. 1 to 5911. It can also contain polynucleotide sequences encoding other polypeptides that enhance, facilitate, or modulate the desired result, such as fusion components that facilitate protein purification, and sequences that increase immunogenicity of the resultant protein or polypeptide.

25 Also embodied in the present invention are host cells transformed with the vectors as described above. Both prokaryotic and eukaryotic host cells may be used. Prokaryotic hosts include bacterial cells, for example *E. coli* and *Mycobacteria*. Among eukaryotic hosts are yeast, insect, avian, plant and mammalian cells. Host systems are known in the art and need not be
30 described in detail herein. Examples of mammalian host cells include but not limited to COS, HeLa, and CHO cells.

The host cells of this invention can be used, inter alia, as repositories of polynucleotides differentially expressed in non-metastatic or metastatic breast tumor cells, or as vehicles for production of the polynucleotides and the encoded polypeptides.

5

Methods of Cloning Novel Transcripts and Genes

As noted above, this invention encompasses genes, either genomic or cDNA, which code for a polypeptide or protein in the cell of interest. The genes specifically hybridize under moderate or stringent conditions to a polynucleotide identified by SEQ ID NOS. 1 through 5911 or their respective complements. The process of identification of larger fragment or the full-length coding sequence to which the partial sequence depicted in SEQ ID NOS. 1 through 5911 hybridizes preferably involves the use of the methods and reagents provided in this invention, either singularly or in combination. The complete coding sequence for the gene (either genomic or cDNA) may be known or novel.

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RACE-PCR Technique

One method to isolate the gene or cDNA which codes for a polypeptide or protein involves the 5'-RACE-PCR technique. In this technique, the poly-A mRNA that contains the coding sequence of particular interest is first identified by hybridization to a sequence disclosed herein and then reverse transcribed with a 3'-primer comprising the sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer of a known sequence, which preferably contains a convenient cloning restriction site attached at the 5' end. The tagged cDNA is then amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, e.g., BRL Life Technologies Inc, Clontech) according to the manufacturer's instructions.

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Isolation of partial cDNA (3' fragment) by 3' directed PCR reaction

This procedure is a modification of the protocol described in Polyak et al. (1997) *Nature* 389:300. Briefly, the procedure uses SAGE tags in PCR
5 reaction such that the resultant PCR product contains the SAGE tag of interest as well as additional cDNA, the length of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source believed to express the cDNA corresponding to a
10 given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-**Biotin**-TCC GGC GCG CCG TTT T CC CAG TCA CGA(30)-
15 3', contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (**B**) for capture to streptavidin-coated magnetic beads, and an *Asc*I restriction endonuclease site for releasing the cDNA from the streptavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region
20 capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

cDNA constructed utilizing this or similar modified oligo-dT primer is then processed exactly as described in U.S. Patent No. 5,695,937 up until adapter ligation where only one adapter is ligated to the cDNA pool. After
25 adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the
30 tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Isolation of cDNA using GeneTrapper or modified GeneTrapper Technology

The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithersburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The target sequence is based on the tag sequence of the present invention. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded target to double-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the ³²P-labeled oligonucleotide as described above for solution hybridization, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

Isolation of cDNAs from a library by probing with the SAGE transcript or tag

Classical methods of constructing cDNA libraries are taught in Sambrook et al., *supra*. Recent procedures described in Velculescu et al. (1997) *Science* 270:484) can be employed to construct an expression cDNA library cloned into the ZAP Express vector. A ZAP Express cDNA synthesis kit is available from Stratagene is used accordingly to the manufacturer's

protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert et al. (1988) *Mol. Cell. Bio.* 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes except that the hybridization temperature is reduced to room temperature. Washes are
5 performed in 6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with ^{32}P -ATP through use of T4 polynucleotide kinase.

Identification of known genes or ESTs

10 In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a databale called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone. Software programs exist (TIGR
15 assembler and TIGEM EST assembly machine and contig assembly program (see Huang X. (1996) *Genomics* 33:21-23)) that allow for assembling ESTs into contiguous sequences from any organism.

Polypeptides of the Invention

20 This invention provides proteins or polypeptides expressed from a polynucleotide of this invention, which is intended to include wild-type and recombinantly produced polypeptides and proteins from procaryotic and eucaryotic host cells, as well as muteins, analogs, fusions and fragments thereof. In some embodiments, the term also includes antibodies and anti-
25 idiotypic antibodies.

It is understood that equivalents or variants of the wild-type polypeptide or protein also are within the scope of this invention. An "equivalent" varies from the wild-type sequence encoded by the polynucleotides of the invention by any combination of additions, deletions, or
30 substitutions while preserving at least one functional property of the fragment relevant to the context in which it is being used. For instance, an equivalent of a polypeptide of the invention may have the ability to elicit an immune

response with a similar antigen specificity as that elicited by the wild-type polypeptide. As is apparent to one skilled in the art, the equivalent may also be associated with, or conjugated with, other substances or agents to facilitate, enhance, or modulate its function.

5 The invention includes modified polypeptides containing conservative or non-conservative substitutions that do not significantly affect their properties, such as the immunogenicity of the peptides or their tertiary structures. Modification of polypeptides is routine practice in the art. Amino acid residues which can be conservatively substituted for one another include
10 but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. These polypeptides also include glycosylated and nonglycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with
15 different sugars, acetylation, and phosphorylation.

 The polypeptides of the invention can also be conjugated to a chemically functional moiety. Typically, the moiety is a label capable of producing a detectable signal. These conjugated polypeptides are useful, for example, in detection systems such as imaging of breast tumor. Such labels
20 are known in the art and include, but are not limited to, radioisotopes, enzymes, fluorescent compounds, chemiluminescent compounds, bioluminescent compounds substrate cofactors and inhibitors. See, for examples of patents teaching the use of such labels, U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and
25 4,366,241. The moieties can be covalently linked to the polypeptides, recombinantly linked, or conjugated to the polypeptides through a secondary reagent, such as a second antibody, protein A, or a biotin-avidin complex.

 Other functional moieties include agents that enhance immunological reactivity, agents that facilitate coupling to a solid support, vaccine carriers,
30 bioresponse modifiers, paramagnetic labels and drugs. Agents that enhance immunological reactivity include, but are not limited to, bacterial superantigens. Agents that facilitate coupling to a solid support include, but

are not limited to, biotin or avidin. Immunogen carriers include, but are not limited to, any physiologically acceptable buffers.

The invention also encompasses fusion proteins comprising polypeptides encoded by the polynucleotides disclosed herein and fragments thereof. Such fusion may be between two or more polypeptides of the invention and a related or unrelated polypeptide. Useful fusion partners include sequences that facilitate the intracellular localization of the polypeptide, or enhance immunological reactivity or the coupling of the polypeptide to an immunoassay support or a vaccine carrier. For instance, the polypeptides can be fused with a bioresponse modifier. Examples of bioresponse modifiers include, but are not limited to, fluorescent proteins such as green fluorescent protein (GFP), cytokines or lymphokines such as interleukin-2 (IL-2), interleukin 4 (IL-4), GM-CSF, and K-interferon. Another useful fusion sequence is one that facilitates purification. Examples of such sequences are known in the art and include those encoding epitopes such as Myc, HA (derived from influenza virus hemagglutinin), His-6, or FLAG. Other fusion sequences that facilitate purification are derived from proteins such as glutathione S-transferase (GST), maltose-binding protein (MBP), or the Fc portion of immunoglobulin. For immunological purposes, tandemly repeated polypeptide segments may be used as antigens, thereby producing highly immunogenic proteins.

The proteins of this invention also can be combined with various liquid phase carriers, such as sterile or aqueous solutions, pharmaceutically acceptable carriers, suspensions and emulsions. Examples of non-aqueous solvents include propyl ethylene glycol, polyethylene glycol and vegetable oils. When used to prepare antibodies, the carriers also can include an adjuvant that is useful to non-specifically augment a specific immune response. A skilled artisan can easily determine whether an adjuvant is required and select one. However, for the purpose of illustration only, suitable adjuvants include, but are not limited to Freund's Complete and Incomplete, mineral salts and polynucleotides.

The proteins and polypeptides of this invention are obtainable by a number of processes well known to those of skill in the art, which include purification, chemical synthesis and recombinant methods. Full-length proteins can be purified from a cell derived from non-metastatic or metastatic breast tumor tissue or tissue lysate by methods such as immunoprecipitation with antibody, and standard techniques such as gel filtration, ion-exchange, reversed-phase, and affinity chromatography using a fusion protein as shown herein. For such methodology, see for example Deutscher et al. (1999) GUIDE TO PROTEIN PURIFICATION: METHODS IN ENZYMOLOGY (Vol. 182, Academic Press). Accordingly, this invention also provides the processes for obtaining these proteins and polypeptides as well as the products obtainable and obtained by these processes.

The proteins and polypeptides also can be obtained by chemical synthesis using a commercially available automated peptide synthesizer such as those manufactured by Perkin Elmer/Applied Biosystems, Inc., Model 430A or 431A, Foster City, CA, USA. The synthesized protein or polypeptide can be precipitated and further purified, for example by high performance liquid chromatography (HPLC). Accordingly, this invention also provides a process for chemically synthesizing the proteins of this invention by providing the sequence of the protein and reagents, such as amino acids and enzymes and linking together the amino acids in the proper orientation and linear sequence.

Alternatively, the proteins and polypeptides can be obtained by well-known recombinant methods as described, for example, in Sambrook et al. (1989) *supra*, using the host cell and vector systems described above.

Antibodies

Also provided by this invention is an antibody capable of specifically binding to the proteins or polypeptides as described above. The antibodies of the present invention encompass polyclonal antibodies and monoclonal antibodies. They include but are not limited to mouse, rat, and rabbit or human antibodies. This invention also encompasses functionally equivalent antibodies and fragments thereof. As used herein with respect to the

exemplified antibodies, the phrase "functional equivalent" means a antibody or fragment thereof, or any molecule having the antigen binding site (or epitope) of the antibody that cross-blocks an exemplified antibody when used in an immunoassay such as immunoblotting or immunoprecipitation.

5 Antibody fragments include the Fab, Fab', F(ab')₂, and Fv regions, or derivatives or combinations thereof. Fab, Fab', and F(ab')₂ regions of an immunoglobulin may be generated by enzymatic digestion of the monoclonal antibodies using techniques well known to those skilled in the art. Fab fragments may be generated by digesting the monoclonal antibody with papain
10 and contacting the digest with a reducing agent to reductively cleave disulfide bonds. Fab' fragments may be obtained by digesting the antibody with pepsin and reductive cleavage of the fragment so produce with a reducing agent. In the absence of reductive cleavage, enzymatic digestion of the monoclonal with pepsin produces F(ab')₂ fragments.

15 It will further be appreciated that encompassed within the definition of antibody fragment is single chain antibody that can be generated as described in U.S. Pat. No. 4,704,692, as well as chimeric antibodies and humanized antibodies (Oi et al. (1986) *BioTechniques* 4(3):214). Chimeric antibodies are those in which the various domains of the antibodies' heavy and light chains
20 are coded for by DNA from more than one species.

As used herein with regard to the monoclonal antibody, the "hybridoma cell line" is intended to include all derivatives, progeny cells of the parent hybridoma that produce the monoclonal antibodies specific for the polypeptides of the present invention, regardless of generation of karyotypic
25 identity.

Laboratory methods for producing polyclonal antibodies and monoclonal antibodies, as well as deducing their corresponding nucleic acid sequences, are known in the art, see Harlow and Lane (1988) *supra* and Sambrook et al. (1989) *supra*. For production of polyclonal antibodies, an
30 appropriate host animal is selected, typically a mouse or rabbit. The substantially purified antigen, whether the whole transmembrane domain, a fragment thereof, or a polypeptide corresponding to a segment of or the entire

specific loop region within the transmembrane domain, coupled or fused to another polypeptide, is presented to the immune system of the host by methods appropriate for the host. The antigen is introduced commonly by injection into the host footpads, via intramuscular, intraperitoneal, or intradermal routes.

5 Peptide fragments suitable for raising antibodies may be prepared by chemical synthesis, and are commonly coupled to a carrier molecule (e.g., keyhole limpet hemocyanin) and injected into a host over a period of time suitable for the production of antibodies. Alternatively, the antigen can be generated recombinantly as a fusion protein. Examples of components for these fusion
10 proteins include, but are not limited to myc, HA, FLAG, His-6, glutathione S-transferase, maltose binding protein or the Fc portion of immunoglobulin.

The monoclonal antibodies of this invention refer to antibody compositions having a homogeneous antibody population. It is not intended to be limited as regards to the source of the antibody or the manner in which it is
15 made. Generally, monoclonal antibodies are biologically produced by introducing protein or a fragment thereof into a suitable host, e.g., a mouse. After the appropriate period of time, the spleens of such animal is excised and individual spleen cells fused, typically, to immortalized myeloma cells under appropriate selection conditions. Thereafter the cells are clonally separated
20 and the supernatants of each clone are tested for their production of an appropriate antibody specific for the desired region of the antigen using methods well known in the art.

The isolation of other hybridomas secreting monoclonal antibodies with the specificity of the monoclonal antibodies of the invention can also be
25 accomplished by one of ordinary skill in the art by producing anti-idiotypic antibodies (Herlyn et al. (1986) *Science* 232:100). An anti-idiotypic antibody is an antibody which recognizes unique determinants present on the monoclonal antibody produced by the hybridoma of interest.

Idiotypic identity between monoclonal antibodies of two hybridomas
30 demonstrates that the two monoclonal antibodies are the same with respect to their recognition of the same epitopic determinant. Thus, by using antibodies to the epitopic determinants on a monoclonal antibody it is possible to identify

other hybridomas expressing monoclonal antibodies of the same epitopic specificity.

It is also possible to use the anti-idiotypic technology to produce monoclonal antibodies which mimic an epitope. For example, an anti-
5 idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the mirror image of the epitope bound by the first monoclonal antibody. Thus, in this instance, the anti-idiotypic monoclonal antibody could be used for immunization for production of these antibodies.

10 Other suitable techniques of antibody production include, but are not limited to, *in vitro* exposure of lymphocytes to the antigenic polypeptides or selection of libraries of antibodies in phage or similar vectors. See Huse et al. (1989) *Science* 246:1275-1281. Genetically engineered variants of the antibody can be produced by obtaining a polynucleotide encoding the
15 antibody, and applying the general methods of molecular biology to introduce mutations and translate the variant. The above described antibody "derivatives" are further provided herein.

Sera harvested from the immunized animals provide a source of polyclonal antibodies. Detailed procedures for purifying specific antibody
20 activity from a source material are known within the art. Undesired activity cross-reacting with other antigens, if present, can be removed, for example, by running the preparation over adsorbants made of those antigens attached to a solid phase and eluting or releasing the desired antibodies off the antigens. If desired, the specific antibody activity can be further purified by such
25 techniques as protein A chromatography, ammonium sulfate precipitation, ion exchange chromatography, high-performance liquid chromatography and immunoaffinity chromatography on a column of the immunizing polypeptide coupled to a solid support.

The specificity of an antibody refers to the ability of the antibody to
30 distinguish polypeptides comprising the immunizing epitope from other polypeptides. An ordinary skill in the art can readily determine without undue experimentation whether an antibody shares the same specificity as a antibody

of this invention by determining whether the antibody being tested prevents an antibody of this invention from binding the polypeptide(s) with which the antibody is normally reactive. If the antibody being tested competes with the antibody of the invention as shown by a decrease in binding by the antibody of
5 this invention, then it is likely that the two antibodies bind to the same or a closely related epitope. Alternatively, one can pre-incubate the antibody of this invention with the polypeptide(s) with which it is normally reactive, and determine if the antibody being tested is inhibited in its ability to bind the antigen. If the antibody being tested is inhibited, then, in all likelihood, it has
10 the same, or a closely related, epitopic specificity as the antibody of this invention.

The antibodies of the invention can be bound to many different carriers. Thus, this invention also provides compositions containing antibodies and a carrier. Carriers can be active and/or inert. Examples of
15 well-known carriers include polypropylene, polystyrene, polyethylene, dextran, nylon, amylases, glass, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding antibodies, or will be able to ascertain such,
20 using routine experimentation.

The antibodies of this invention can also be conjugated to a detectable agent or a hapten. The complex is useful to detect the polypeptide(s) (or polypeptide fragments) to which the antibody specifically binds in a sample, using standard immunochemical techniques such as immunohistochemistry as
25 described by Harlow and Lane (1988). *supra*. There are many different labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include radioisotopes, enzymes, colloidal metals, fluorescent compounds, bioluminescent compounds, and chemiluminescent compounds. Those of
30 ordinary skill in the art will know of other suitable labels for binding to the antibody, or will be able to ascertain such, using routine experimentation.

Furthermore, the binding of these labels to the antibody of the invention can be done using standard techniques common to those of ordinary skill in the art.

Another technique which may also result in greater sensitivity consists of coupling the antibodies to low molecular weight haptens. These haptens
5 can then be specifically detected by means of a second reaction. For example, it is common to use such haptens as biotin, which reacts avidin, or dinitrophenyl, pyridoxal, and fluorescein, which can react with specific anti-hapten antibodies. See Harlow and Lane (1988) *supra*.

Compositions containing the antibodies, fragments thereof or cell lines
10 which produce the antibodies, are encompassed by this invention. When these compositions are to be used pharmaceutically, they are combined with a pharmaceutically acceptable carrier.

Uses of polynucleotides, polypeptides and antibodies of the present 15 invention

The polynucleotides, polypeptides and antibodies embodied in this invention provide specific reagents that can be used in standard diagnostic procedures. Accordingly, one embodiment of the present invention is a method of diagnosing the metastatic condition of a breast cell by detecting
20 differential expression of a polynucleotide comprising any one of the sequences listed in SEQ ID NOS. 1 to 5911, or 1-3175 or 3176-5911, or the populations identified above, or the encoded polypeptide(s). The method can be used for aiding in the diagnosis of metastatic breast cancer by detecting a genotype that is correlated with a phenotype characteristic of metastatic breast
25 tumor cells.

In one aspect, overexpression of a polynucleotide identified in Table 2 or comprising or corresponding to Seq. ID No. 3176-5911 is indicative of the non-metastatic state of a breast cell. Conversely, overexpression of a polynucleotide comprising the sequence selected from polynucleotide (e.g.,
30 identified in Table 1 or comprising or corresponding to Seq. ID No. 1 to 3175) is indicative of the non-metastatic state of a breast cell.

In yet another aspect, the differential expression of the polynucleotides is determined by assaying for a difference, between the non-metastatic and metastatic breast tumor cells, in the level of transcripts that specifically hybridize with one or more of the exemplified sequences. In another aspect, the differential expression of the polynucleotides is determined by detecting a difference in the level of the encoded polypeptides.

Cell or tissue samples used for this invention encompass body fluid, solid tissue samples, tissue cultures or cells derived therefrom and the progeny thereof, and sections or smears prepared from any of these sources, or any other samples that may contain a breast cell having the polynucleotides disclosed herein or their gene products.

In assaying for an alteration in mRNA level, nucleic acid contained in the aforementioned samples is first extracted according to standard methods in the art. For instance, mRNA can be isolated using various lytic enzymes or chemical solutions according to the procedures set forth in Sambrook et al. (1989), *supra* or extracted by nucleic-acid-binding resins following the accompanying instructions provided by manufactures. The mRNA contained in the extracted nucleic acid sample is then detected by hybridization (e.g. Northern blot analysis) and/or amplification procedures according to methods widely known in the art or based on the methods exemplified herein.

Nucleic acid molecules having at least 10 nucleotides and exhibiting sequence complementarity or homology to the polynucleotides described herein find utility as hybridization probes. It is known in the art that a "perfectly matched" probe is not needed for a specific hybridization. Minor changes in probe sequence achieved by substitution, deletion or insertion of a small number of bases do not affect the hybridization specificity. In general, as much as 20% base-pair mismatch (when optimally aligned) can be tolerated. Preferably, a probe useful for detecting the aforementioned mRNA that is differentially expressed in non-metastatic or metastatic breast tissues is at least about 80% identical to the homologous region of comparable size contained in the sequences to be detected. More preferably, the probe is 85% identical to the corresponding gene sequence after alignment of the homologous region;

even more preferably, it exhibits 90% identity. Specifically, a preferred probe is selected from the group of SEQ ID NOS. 1 to 5911, or their respective complements.

These probes can be used in hybridization reaction (*e.g.* Southern and Northern blot analysis) to detect, prognose, diagnose or monitor the metastatic states associated with the differential expression of these genes. The total size of fragment, as well as the size of the complementary stretches, will depend on the intended use or application of the particular nucleic acid segment. Smaller fragments derived from the known sequences will generally find use in hybridization embodiments, wherein the length of the complementary region may be varied, such as between about 10 and about 100 nucleotides, or even full length according to the complementary sequences one wishes to detect.

Nucleotide probes having complementary sequences over stretches greater than 10 nucleotides in length are generally preferred, so as to increase stability and selectivity of the hybrid, and thereby improving the specificity of particular hybrid molecules obtained. More preferably, one can design nucleic acid molecules having gene-complementary stretches of more than 50 nucleotides in length, or even longer where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCRTM technology with two priming oligonucleotides as described in U.S. Pat. No. 4,603,102 or by introducing selected sequences into recombinant vectors for recombinant production. A preferred probe is about 50-75 or more preferably, 50-100, nucleotides in length.

In certain embodiments, it will be advantageous to employ nucleic acid sequences of the present invention in combination with an appropriate means, such as a label, for detecting hybridization and therefore complementary sequences. A wide variety of appropriate indicator means are known in the art, including fluorescent, radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred embodiments, one will likely desire to employ a fluorescent label or an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of

radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with complementary
5 nucleic acid-containing samples.

The nucleotide probes of the present invention can also be used as primers and detection of genes or gene transcripts that are differentially expressed in certain body tissues. A preferred primer is one comprising a sequence of SEQ ID NOS. 1 through 5911 or their respective complements.
10 Additionally, a primer useful for detecting the aforementioned gene or transcript is at least about 80% identical to the homologous region of comparable size of the gene or transcript to be detected contained in the previously identified sequences. For the purpose of this invention, amplification means any method employing a primer-dependent polymerase
15 capable of replicating a target sequence with reasonable fidelity. Amplification may be carried out by natural or recombinant DNA-polymerases such as T7 DNA polymerase, Klenow fragment of *E.coli* DNA polymerase, and reverse transcriptase.

A preferred amplification method is PCR. General procedures for PCR
20 are taught in MacPherson et al., PCR: A PRACTICAL APPROACH, (IRL Press at Oxford University Press (1991)). However, PCR conditions used for each application reaction are empirically determined. A number of parameters influence the success of a reaction. Among them are annealing temperature and time, extension time, Mg^{2+} ATP concentration, pH, and the relative
25 concentration of primers, templates, and deoxyribonucleotides.

After amplification, the resulting DNA fragments can be detected by agarose gel electrophoresis followed by visualization with ethidium bromide staining and ultraviolet illumination. A specific amplification of the gene or transcript of interest can be verified by demonstrating that the amplified DNA
30 fragment has the predicted size, exhibits the predicated restriction digestion pattern, and/or hybridizes to the correct cloned DNA sequence.

The probes also can be attached to a solid support for use in high throughput screening assays using methods known in the art. PCT WO 97/10365 and U.S. Patent numbers 5,405,783, 5,412,087 and 5,445,934, for example, disclose the construction of high density oligonucleotide chips which
5 can contain one or more of the sequences disclosed herein. Based in the methods disclosed in U.S. Patent numbers 5,405,783, 5,412,087 and 5,445,934, the probes of this invention are synthesized on a derivatized glass surface. Photoprotected nucleoside phosphoramidites are coupled to the glass surface, selectively deprotected by photolysis through a photolithographic
10 mask, and reacted with a second protected nucleoside phosphoramidite. The coupling/deprotection process is repeated until the desired probe is complete.

The expression level of a gene of interest is determined through exposure of a nucleic acid sample to the probe-modified chip. Extracted nucleic acid is labeled, for example, with a fluorescent tag, preferably during
15 an amplification step. Hybridization of the labeled sample is performed at an appropriate stringency level. The degree of probe-nucleic acid hybridization is quantitatively measured using a detection device, such as a confocal microscope. See U.S. Pat Nos. 5,578,832 and 5,631,734. The obtained measurement is directly correlated with gene expression level.

20 More specifically, the probes and high density oligonucleotide probe arrays provide an effective means of monitoring expression of a multiplicity of genes. The expression monitoring methods of this invention may be used in a wide variety of circumstances including detection of disease, identification of differential gene expression between two samples, or screening for
25 compositions that upregulate or downregulate the expression of particular genes.

In another preferred embodiment, the methods of this invention are used to monitor expression of the genes which specifically hybridize to the probes of this invention in response to defined stimuli, such as a drug.

30 In one embodiment, the hybridized nucleic acids are detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill

in the art. However, in one aspect, the label is simultaneously incorporated during the amplification step in the preparation of the sample nucleic acid.

Thus, for example, polymerase chain reaction (PCR) with labeled primers or labeled nucleotides will provide a labeled amplification product. In a separate
5 embodiment, transcription amplification, as described above, using a labeled nucleotide (e.g. fluorescein-labeled UTP and/or CTP) incorporates a label in to the transcribed nucleic acids.

Alternatively, a label may be added directly to the original nucleic acid sample (e.g., mRNA, polyA, mRNA, cDNA, etc.) or to the amplification
10 product after the amplification is completed. Means of attaching labels to nucleic acids are well known to those of skill in the art and include, for example nick translation or end-labeling (e.g. with a labeled RNA) by kinasing of the nucleic acid and subsequent attachment (ligation) of a nucleic acid linker joining the sample nucleic acid to a label (e.g., a fluorophore).

15 The nucleic acid sample also may be modified prior to hybridization to the high density probe array in order to reduce sample complexity thereby decreasing background signal and improving sensitivity of the measurement using the methods disclosed in WO 97/10365.

Results from the chip assay are typically analyzed using a computer
20 software program. See, for example, EP 0717 113 A2 and WO 95/20681. The hybridization data are read into the program, which calculates the expression level of the targeted gene(s). This figure is compared against existing data sets of gene expression levels for diseased and healthy individuals. A correlation between the obtained data and that of a set of diseased individuals having non-
25 metastatic or metastatic breast cancer indicates the neoplastic stage of the tested tumor sample.

Expression of the genes associated with breast cancer progression can also be determined by examining the protein product of the polynucleotides of the present invention. Determining the protein level involves a) providing a
30 biological sample containing polypeptides; and (b) measuring the amount of any immunospecific binding that occurs between an antibody reactive to the

protein products of interest and a component in the sample, in which the amount of immunospecific binding indicates the level of the protein products.

A variety of techniques are available in the art for protein analysis.

They include but are not limited to radioimmunoassays, ELISA (enzyme
5 linked immunoradiometric assays), "sandwich" immunoassays, immunoradiometric assays, in situ immunoassays (using *e.g.*, colloidal gold, enzyme or radioisotope labels), western blot analysis, immunoprecipitation assays, immunofluorescent assays, and SDS-PAGE. In addition, cell sorting analysis can be employed to detect cell surface antigens. Such analysis
10 involves labeling target cells with antibodies coupled to a detectable agent, and then separating the labeled cells from the unlabeled ones in a cell sorter. A sophisticated cell separation method is fluorescence-activated cell sorting (FACS). Cells traveling in single file in a fine stream are passed through a laser beam, and the fluorescence of each cell bound by the fluorescently
15 labeled antibodies is then measured.

Antibodies that specifically recognize and bind to the protein products of interest are required for conducting the aforementioned protein analyses. These antibodies may be purchased from commercial vendors or generated and screened using methods well known in the art. See Harlow and Lane (1988)
20 *supra.* and Sambrook et al. (1989) *supra.*

In diagnosing malignancy or metastasis characterized by a differential expression of genes or transcripts that are associated with either the non-metastatic or metastatic state of a breast cell, one typically conducts a comparative analysis of the subject and appropriate controls. Preferably, a
25 diagnostic test includes a control sample derived from a subject (hereinafter positive control), that exhibits a detectable increase in expression of the genes, preferably at a level of 3 folds or more and clinical characteristics of tumor metastasis. More preferably, a diagnosis also includes a control sample derived from a subject (hereinafter negative control), that lacks the clinical
30 characteristics of the metastatic state and whose expression level of the gene at question is within a normal range. A positive correlation between the subject and the positive control with respect to the identified differential gene

expression indicates the presence or a predisposition of metastatic breast cancer. A lack of correlation between the subject and the negative control confirms the diagnosis.

5 The selection of an appropriate control cell or tissue is dependent on the sample cell or tissue initially selected and its phenotype which is under investigation. Whereas the sample cell is derived from a metastatic breast tumor tissue, one or more counterpart non-metastatic cells of the sample cells can be used as control cells. Counterparts would include, for example, cell lines established from the same or related cells to those found in the sample
10 cell population. Preferably, a control matches the tissue, and/or cell type the tested sample is derived from. More preferably, a control is derived from a primary breast tumor of the same individual from whom the test sample is derived. It is also preferable to analyze the control and the tested sample in parallel.

15 There are various methods available in the art for quantifying mRNA or protein level from a cell sample and indeed, any method that can quantify these levels is encompassed by this invention. For example, determination of the mRNA level of the gene may involve, in one aspect, measuring the amount of mRNA in a mRNA sample isolated from the breast cell by hybridization or
20 quantitative amplification using at least one oligonucleotide probe that is complementary to the mRNA. Determination of the aforementioned protein products requires measuring the amount of immunospecific binding that occurs between an antibody reactive to the product of interest. To detect and quantify the immunospecific binding, or signals generated during
25 hybridization or amplification procedures, digital image analysis systems including but not limited to those that detect radioactivity of the probes or chemiluminescence can be employed.

Screening Assays

30 The present invention also provides a screen for various agents which modulate the expression of a polynucleotide associated the metastatic condition of a breast cell by first contacting a cell with an effective amount of

- a potential agent, and then assaying for a change in the expression level of a polynucleotide selected from the populations identified above. A change in the expression level is indicative of a candidate therapeutic agent. Preferably, the agent when administered into a cell or subject reduces the level of
- 5 expression of a gene or transcript that is associated with breast cancer progression and is further characterized as comprising a sequence selected from SEQ ID NO. 1 through 3175. A preferred agent may also enhance expression of genes or transcripts comprising a sequence of SEQ ID NOS. 3176 to 5911. In certain aspects of the invention, an agent may result in
- 10 phenotypic changes of the recipient cell as evidenced by an agent-induced cell apoptosis, a reduced rate of cell growth or cell motility. Altered gene expression can be detected by assaying for altered mRNA expression or protein expression using the probes, primers and antibodies as described herein.
- 15 To practice the method *in vitro*, suitable cell cultures or tissue cultures from metastatic breast cells are first provided. The cell can be a cultured cell or a genetically modified cell in which a transcript from SEQ ID NOS. 1 through 5911, or their complements, or alternatively, transcripts which contain or correspond to a tag or its respective complement is expressed.
- 20 Alternatively, the cells can be from a tissue biopsy. The cells are cultured under conditions (temperature, growth or culture medium and gas (CO₂)) and for an appropriate amount of time to attain exponential proliferation without density dependent constraints. It also is desirable to maintain an additional separate cell culture; one which does not receive the agent being tested as a
- 25 control.

As is apparent to one of skill in the art, suitable cells may be cultured in microtiter plates and several agents may be assayed at the same time by noting genotypic changes and/or phenotypic changes.

- When the agent is a composition other than naked DNA or RNA, the
- 30 agent may be directly added to the cell culture or added to culture medium for addition. As is apparent to those skilled in the art, an "effective" amount must be added which can be empirically determined. When the agent is a

polynucleotide, it may be introduced directly into a cell by transfection or electroporation. Alternatively, it may be inserted into the cell using a gene delivery vehicle or other methods as described above.

For the purposes of this invention, an "agent" is intended to include,
5 but not be limited to a biological or chemical compound such as a simple or complex organic or inorganic molecule, a peptide, a protein (e.g. antibody) or a polynucleotide (e.g. anti-sense). A vast array of compounds can be synthesized, for example polymers, such as polypeptides and polynucleotides, and synthetic organic compounds based on various core structures, and these
10 are also included in the term "agent". In addition, various natural sources can provide compounds for screening, such as plant or animal extracts, and the like. It should be understood, although not always explicitly stated that the agent is used alone or in combination with another agent, having the same or different biological activity as the agents identified by the inventive screen.
15 The agents and methods also are intended to be combined with other therapies.

The assays also can be performed in a subject. When the subject is an animal such as a rat, mouse or simian, the method provides a convenient animal model system which can be used prior to clinical testing of an agent. In this system, a candidate agent is a potential drug if transcript expression is
20 altered, i.e., upregulated (such as restoring tumor suppressor function), downregulated or eliminated as with drug resistant genes or oncogenes, or if symptoms associated or correlated to the presence of cells containing transcript expression are ameliorated, each as compared to untreated, animal having the pathological cells. It also can be useful to have a separate negative control
25 group of cells or animals which are healthy and not treated, which provides a basis for comparison. After administration of the agent to subject, suitable cells or tissue samples are collected and assayed for altered gene expression.

As an example of an animal model, groups of nude mice (Balb/c NCR nu/nu female, Simonsen, Gilroy, CA) are each subcutaneously inoculated with
30 about 10^5 to about 10^9 hyperproliferative, cancer or target cells as defined herein. When the tumor is established, the agent is administered, for example, by subcutaneous injection around the tumor. Tumor measurements to

determine reduction of tumor size are made in two dimensions using venier calipers twice a week. Other animal models may also be employed as appropriate.

These agents of this invention and the above noted compounds and their derivatives can be combined with a pharmaceutically acceptable carrier for the preparation of medicaments for use in the methods described herein. They can be administered to treat a cancerous condition, or to prevent progression from a pre-neoplastic or non-metastatic state into a neoplastic or a metastatic state.

10 In a preferred embodiment, an agent of the present invention is administered to reverse the metastatic condition of a breast cell. As used herein, the term "reversing the metastatic condition" of a cell is intended to include apoptosis, necrosis or any other means of preventing cell division, reduced cell motility, loss of pharmaceutical resistance, maturation, differentiation or reversion of any other metastatic phenotypes. For example, characteristics associated with a metastatic phenotype (a set of *in vitro* characteristics associated with a tumorigenic ability *in vivo*) include but are not limited to a more rounded cell morphology, looser substratum attachment, loss of contact inhibition, and loss of anchorage dependence.

20 One can determine if reversion of the metastatic condition of a breast cell is achieved by performing assays standard in the art. For example, cell proliferation can be assayed by measuring ³H-thymidine incorporation, by direct cell count, by detecting changes in transcriptional activity of known genes such as proto-oncogenes (e.g., fos, myc) or cell cycle markers; cell viability can be assessed by staining cells with a dye that reacts with either living or dead cells; cellular differentiation can be monitored by histological methods or by detecting the presence or loss of certain surface markers that are associated with undifferentiated or differentiated phenotype; cell motility can be assayed directly by measuring the cell migration speed, or indirectly by determining the fraction of cells developed lamellipodia.

The agents of the present invention can be administered to a cell or a subject by various delivery systems known in the art. Non-limiting examples

include encapsulation in liposomes, microparticles, microcapsules, expression by recombinant cells, receptor-mediated endocytosis (see, *e.g.*, Wu and Wu (1987) *J. Biol. Chem.* 262:4429-4432), and construction of a therapeutic nucleic acid as part of a retroviral or other vector. Methods of delivery include
5 but are not limited to transdermally, gene therapy, intra-arterial, intra-muscular, intravenous, intranasal, and oral routes, and include sustained delivery systems. In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation,
10 local infusion during surgery, by injection, or by means of a catheter or targeted gene delivery of the sequence coding for the therapeutic.

The agents identified herein as effective for their intended purpose can be administered to subjects or individuals susceptible to or at risk of developing breast cancer. When the agent is administered to a subject such as
15 a mouse, a rat or a human patient, the agent can be added to a pharmaceutically acceptable carrier and systemically or topically administered to the subject. Therapeutic amounts can be empirically determined and will vary with the pathology being treated, the subject being treated and the efficacy and toxicity of the agent.

20 Administration *in vivo* can be effected in one dose, continuously or intermittently throughout the course of treatment. Methods of determining the most effective means and dosage of administration are well known to those of skill in the art and will vary with the composition used for therapy, the purpose of the therapy, the target cell being treated, and the subject being treated.
25 Single or multiple administrations can be carried out with the dose level and pattern being selected by the treating physician. Suitable dosage formulations and methods of administering the agents can be found below.

The agents and compositions of the present invention can be used in the manufacture of medicaments and for the treatment of humans and other
30 animals by administration in accordance with conventional procedures, such as an active ingredient in pharmaceutical compositions.

The pharmaceutical compositions can be administered orally, intranasally, parenterally, transdermally or by inhalation therapy, and may take the form of tablets, lozenges, granules, capsules, pills, ampoules, suppositories or aerosol form. They may also take the form of gene therapy, suspensions, solutions and emulsions of the active ingredient in aqueous or nonaqueous diluents, syrups, granulates or powders. In addition to an agent of the present invention, the pharmaceutical compositions can also contain other pharmaceutically active compounds or a plurality of compounds of the invention.

It should be understood that in addition to the ingredients particularly mentioned above, the formulations of this invention may include other agents conventional in the art having regard to the type of formulation in question, for example, those suitable for oral administration may include such further agents as sweeteners, thickeners and flavoring agents. It also is intended that the agents, compositions and methods of this invention be combined with other suitable compositions and therapies.

Non-Human Transgenic Animals

In another aspect, the novel polynucleotide sequences associated with non-metastatic and metastatic breast cancer can be used to generate transgenic animal models. In recent years, geneticists have succeeded in creating transgenic animals, for example mice, by manipulating the genes of developing embryos and introducing foreign genes into these embryos. Once these genes have integrated into the genome of the recipient embryo, the resulting embryos or adult animals can be analyzed to determine the function of the gene. The mutant animals are produced to understand the function of known genes *in vivo* and to create animal models of human diseases. (*see, e.g., Chisaka et al. (1992) 355:516-520; Joyner et al. (1992) in POSTIMPLANTATION DEVELOPMENT IN THE MOUSE (Chadwick and Marsh, eds., John Wiley & Sons, United Kingdom) pp:277-297; Dorin et al. (1992) Nature 359:211-215).*

Genomics Applications

A cell's transcriptome offers a snapshot of all expressed genes and their relative level of expression. This information provides a library for the study of the number and types of genes whose transcription is induced or regulated during cell processes such as activation, differentiation, aging, viral transformation, morphogenesis, and mitosis. A comparison of the transcriptomes of a particular cell at various times during the life of the cell, under the same or different environmental stimuli, provides insight into the regulatory process of the cell. Using the transcripts provided herein, the analysis of these and other cellular processes and the effects of environmental stimuli on the cell is possible.

This invention also provides a process for preparing a database for the analysis of a cell's expressed genes by storing in a digital storage medium information related to the sequences of the transcriptome. Using this method, a data processing system for standardized representation of the expressed genes of a cell is compiled. The data processing system is useful to analyze gene expression between two cells by first selecting a cell and then identifying and sequencing the transcriptome of the cell. This information is stored in a computer-readable storage medium as the transcriptome. The transcriptome is then compared with at least one sequence(s) of transcription fragments from a reference cell. The compared sequences are then analyzed. Uniquely expressed sequences and sequences differentially expressed between the reference cell and the selected cell can be identified by this method.

In other words, this invention provides a computer based method for screening the homology of an unknown DNA or mRNA sequence against the complete set of expressed genes of a preselected cell by first providing the complete set of expressed genes, i.e., the transcriptome, in computer readable form and homology screening the DNA or mRNA of the unknown sequence against transcriptome and determining whether the DNA sequence of the unknown contains similarities to any portion of the transcriptome listed in the computer readable form.

Thus, the information provided herein also provides a means to compare the relative abundance of gene transcripts in different biological specimens by use of high-throughput sequence-specific analysis of individual RNAs or their corresponding cDNAs using a modification of the systems
5 described in WO 95/2068, 96/23078 and 5,618,672.

The tags or transcripts also can be attached to a solid support for use in high throughput screening assays. PCT WO 97/10365, for example, discloses the construction of high density oligonucleotide chips. See also, U.S. Pat. Nos. 5,405,783, 5,412,087 and 5,445,934. Using this method, the probes are
10 synthesized on a derivatized glass surface. Photoprotected nucleoside phosphoramidites are coupled to the glass surface, selectively deprotected by photolysis through a photolithographic mask, and reacted with a second protected nucleoside phosphoramidite. The coupling/deprotection process is repeated until the desired probe is complete.

15 The expression level of a gene is determined through exposure of a nucleic acid sample to the probe-modified chip. Extracted nucleic acid is labeled, for example, with a fluorescent tag, preferably during an amplification step. Hybridization of the labeled sample is performed at an appropriate stringency level. The degree of probe-nucleic acid hybridization is
20 quantitatively measured using a detection device, such as a confocal microscope. See U.S. Pat Nos. 5,578,832 and 5,631,734. The obtained measurement is directly correlated with gene expression level.

Results from the chip assay are typically analyzed using a computer software program. See, for example, EP 0717 113 A2 and WO 95/20681. The
25 hybridization data is read into the program, which calculates the expression level of the targeted gene(s). This figure is compared against existing data sets of gene expression levels for that cell type.

For example, the database and methods of using the database provides a means to differentiate normal metastatic from pleural effusion cells from
30 abnormal metastatic from pleural effusion cells. It also allows one to differentiate between metastatic from pleural effusion cells biopsied from different regions from a patient or subject or gene expression before or after

treatment with a potential therapeutic agent. It can be used to analyze drug toxicity and efficacy, as well as to selectively look at protein categories which are expected to be affected by a drug or which may be overexpressed as a result of treatment with a drug, such as the various multi-drug resistant genes.

- 5 Additional utilities of the database include, but are not limited to analysis of the developmental state of a test cell, the influence of viral or bacterial infection, control of cell cycle, effect of a tumor suppressor gene or lack thereof, polymorphism within the cell type, apoptosis, and the effect of regulatory genes.

10

Vaccines for Cancer Treatment and Prevention

- In one embodiment, the present invention comprises vaccines for cancer treatment. Recent advances in vaccine adjuvants provide effective means of administering peptides so that they impact maximally on the immune system. Del-Giudice (1994) *Experientia* 50:1061-1066. A polynucleotide encoding the antigenic peptide also can be administered as a cancer vaccine. The polynucleotide can be administered as naked DNA or alternatively, in expression vectors. Therapy can be enhanced by coadministration of cytokines and/or co-stimulatory molecules which in turn, can be administered as proteins or the polynucleotides encoding the proteins.

20

Host Cells comprising Antigenic Peptides of the Invention

- The invention further provides isolated host cells comprising antigenic peptides of the invention. In some embodiments, these host cells present one or more peptides of the invention on the surface of the cell in the context of an MHC molecule, i.e., an antigenic peptide of the invention is bound to a cell surface MHC molecule such that the peptide can be recognized by an immune effector cell. Isolated host cells which present the polypeptides of this invention in the context of MHC molecules are further useful to expand and isolate a population of educated, antigen-specific immune effector cells. The immune effector cells, e.g., cytotoxic T lymphocytes, are produced by culturing naïve immune effector cells with antigen-presenting cells which

25

30

present the polypeptides in the context of MHC molecules on the surface of the APCs. The population can be purified using methods known in the art, e.g., FACS analysis or FICOLL™ gradient. The methods to generate and culture the immune effector cells as well as the populations produced thereby also are the inventors' contribution and invention. Pharmaceutical compositions comprising the cells and pharmaceutically acceptable carriers are useful in adoptive immunotherapy. Prior to administration *in vivo*, the immune effector cells are screened *in vitro* for their ability to lyse melanoma tumor cells.

10

Gene transfer

Vectors useful in genetic modification

In one embodiment, the present invention provides methods of eliciting efficient antigen-specific immune response in a subject by introducing to the subject recombinant polynucleotides encoding antigenic peptides alone or in combination with immunostimulatory factors. Methods and materials for gene transfer are known in the art, including, for example, viral mediated gene transfer, lipofection, transformation, transfection and transduction. The polynucleotides encoding the immunostimulatory factor and target antigenic peptide can be introduced *ex vivo* into a host cell, for example, dendritic cells. The genetically modified host cells can be introduced as a cell-based vaccine into the target subject. Alternatively, the polynucleotides encoding the immunostimulatory factor and target antigenic peptide can be introduced directly into the subject in the form of gene-based vaccine.

20

Various viral infection techniques have been developed which utilize recombinant viral vectors for gene delivery, and constitute preferred approaches to the present invention. The viral vectors which have been used in gene transfer include, but not limited to, viral sequences derived from simian virus 40 (SV40), adenovirus, adeno-associated virus (AAV), and retroviruses.

30

Vector Transduction of Cells such as APCs

APCs can be transduced with viral vectors encoding a relevant polypeptides. The most common viral vectors include recombinant poxviruses such as vaccinia and fowlpox virus (Bronte et al. (1997) Proc. Natl. Acad. Sci. USA 94:3183-3188; Kim et al. (1997) J. Immunother. 20:276-286) and, preferentially, adenovirus (Arthur et al. (1997) J. Immunol. 159:1393-1403; Wan et al. (1997) Human Gene Therapy 8:1355-1363; Huang et al. (1995) J. Virol. 69:2257-2263). Retrovirus also may be used for transduction of human APCs (Marin et al. (1996) J. Virol. 70:2957-2962).

10 *In vitro* or *ex vivo* exposure of human DCs to adenovirus (Ad) vector at a multiplicity of infection (MOI) of 500 for 16-24 h in a minimal volume of serum-free medium reliably gives rise to foreign polynucleotide expression in 90-100% of DCs. The efficiency of transduction of DCs or other APCs can be assessed by immunofluorescence using fluorescent antibodies specific for the tumor antigen being expressed (Kim et al. (1997) J. Immunother. 20:276-286). Alternatively, the antibodies can be conjugated to an enzyme (e.g. HRP) giving rise to a colored product upon reaction with the substrate. The actual amount of antigenic polypeptides being expressed by the APCs can be evaluated by ELISA.

20 *In vivo* transduction of DCs, or other APCs, can be accomplished by administration of Ad (or other viral vectors) via different routes including intravenous, intramuscular, intranasal, intraperitoneal or cutaneous delivery. The preferred method is cutaneous delivery of Ad vector at multiple sites using a total dose of approximately 1×10^{10} - 1×10^{12} i.u. Levels of *in vivo* transduction can be roughly assessed by co-staining with antibodies directed against APC marker(s) and the antigen being expressed. The staining procedure can be carried out on biopsy samples from the site of administration or on cells from draining lymph nodes or other organs where APCs (in particular DCs) may have migrated (Condon et al. (1996) Nature Med. 2:1122-1128; Wan et al. (1997) Human Gene Therapy 8:1355-1363). The amount of antigen being expressed at the site of injection or in other organs where

transduced APCs may have migrated can be evaluated by ELISA on tissue homogenates.

Although viral gene delivery is more efficient, DCs can also be transduced *in vitro/ex vivo* by non-viral gene delivery methods such as electroporation, calcium phosphate precipitation or cationic lipid/plasmid DNA complexes (Arthur et al. (1997) Cancer Gene Therapy 4:17-25). Transduced APCs can subsequently be administered to the host via an intravenous, subcutaneous, intranasal, intramuscular or intraperitoneal route of delivery.

In vivo transduction of DCs, or other APCs, can potentially be accomplished by administration of cationic lipid/plasmid DNA complexes delivered via the intravenous, intramuscular, intranasal, intraperitoneal or cutaneous route of administration. Gene gun delivery or injection of naked plasmid DNA into the skin also leads to transduction of DCs (Condon et al. (1996) Nature Med. 2:1122-1128 and Raz et al. (1994) Proc. Natl. Acad. Sci. USA 91:9519-9523). Intramuscular delivery of plasmid DNA may also be used for immunization (Rosato et al. (1997) Human Gene Therapy 8:1451-1458).

The transduction efficiency and levels of foreign polynucleotide expression can be assessed as described above for viral vectors.

Administration of Cell-Based Vaccine to Subject

Genetically modified cells can subsequently be administered to the host subject via various routes, including, for example, intravenous infusion, subcutaneous injection, intranasal, intramuscular or intraperitoneal delivery. The cells containing the recombinant polynucleotides may be used to confer immunity to individuals. Administration *in vivo* can be effected in one dose, continuously or intermittently throughout the course of treatment. Methods of determining the most effective means and dosage of administration are well known to those of skill in the art and will vary with the composition used for therapy, the purpose of the therapy, the target cell being treated, and the

subject being treated. Single or multiple administrations can be carried out with the dose level and pattern being selected by the treating physician.

Adoptive Immunotherapy Methods

5 Expanded populations of antigen-specific immune effector cells and APCs presenting antigens find use in adoptive immunotherapy regimes.

 Adoptive immunotherapy methods involve, in one aspect, administering to a subject a substantially pure population of educated, antigen-specific immune effector cells made by culturing naïve immune effector cells
10 with APCs as described above. In some embodiments, the APCs are dendritic cells.

 In one embodiment, the adoptive immunotherapy methods described herein are autologous. In this case, the APCs are made using parental cells isolated from a single subject. The expanded population also employs T cells
15 isolated from that subject. Finally, the expanded population of antigen-specific cells is administered to the same patient.

 In a further embodiment, APCs or immune effector cells are administered with an effective amount of a stimulatory cytokine, such as IL-2 or a co-stimulatory molecule.

20

Immune Effector Cells

 The present invention makes use of antigen-presenting matrices, including APCs, to stimulate production of an enriched population of antigen-specific immune effector cells. Accordingly, the present invention provides a
25 population of cells enriched in educated, antigen-specific immune effector cells, specific for an antigenic peptide of the invention. These cells can cross-react with (bind specifically to) antigenic determinants (epitopes) on natural (endogenous) antigens. In some embodiments, the natural antigen is on the surface of tumor cells and the educated, antigen-specific immune effector cells
30 of the invention suppress growth of the tumor cells. When APCs are used, the antigen-specific immune effector cells are expanded at the expense of the APCs, which die in the culture. The process by which naïve immune effector

cells become educated by other cells is described essentially in Coulie (1997) Molec. Med. Today 3:261-268.

An effector cell population suitable for use in the methods of the present invention can be autogeneic or allogeneic, preferably autogeneic.

- 5 When effector cells are allogeneic, preferably the cells are depleted of alloreactive cells before use. This can be accomplished by any known means, including, for example, by mixing the allogeneic effector cells and a recipient cell population and incubating them for a suitable time, then depleting CD69⁺ cells, or inactivating alloreactive cells, or inducing anergy in the alloreactive
10 cell population.

Hybrid immune effector cells can also be used. Immune effector cell hybrids are known in the art and have been described in various publications. See, for example, International Patent Application Nos. WO 98/46785; and WO 95/16775.

- 15 The following examples are intended to illustrate, but not limit, the invention.

Examples

SAGE Analysis

- 20 A comparative analysis of transcripts expressed in metastatic and primary breast tissues from the same individual was performed by Serial Analysis of Gene Expression ("SAGE") (U.S. Patent No. 5,695,937). Briefly, the SAGE analysis began with providing complementary deoxyribonucleic acid (cDNA) from (1) the metastatic population and (2) non-metastatic
25 population of cells. cDNAs derived from both cell populations were linked to primer sites. Sequence tags were then created, for example, using the appropriate primers to amplify the DNA. By measuring the differences in these tags between the two cell populations, sequences which are preferentially expressed in one but not the other cell type were identified.

Identifying Genes and ESTs Starting from SAGE tags

The primary sequence data were evaluated from the raw concatamer sequences, to count the occurrence of each tag, and provide a report tabulating
5 each SAGE tag and its expression level. Table 2 summarizes the tags corresponding to distinct genes that are preferentially expressed in the primary breast tumor tissue, and Table 1 summarizes the gene sequences that are preferentially expressed in the metastatic breast tumor tissue. Sequence comparison of the tags identified a highly expressed gene, prohibitin as is an
10 anti-proliferative factor (see a review by McClung et al. (1995) *Exp. Gerontol* 30: 99) and loss of this activity has been documented to occur during the progression of breast cancer (Sato et al. (1992) *Cancer Research* 52: 1643).

Of the tags found to be overexpressed in the metastatic breast tissue, many of them were found to match with a known gene sequence. Among
15 them are DNA replication licensing factor that is known to be involved in cell proliferation, and adhesion molecules like p-cadherin that may contribute to the invasiveness of tumor cells. These genes are thus candidate therapeutic targets; down-regulation of their activities may inhibit or prevent cancer metastasis. Many of the tags were not found to match to any known genes or
20 ESTs after searching gene databases. These tags identify novel tags or transcripts or genes and are identified in the column "description" as having "nm" (no match) or having a blank space therein.

While the above description is used to identify human genes, it should be noted that the same procedure has been used for numerous other organisms
25 (rat, mouse, etc), anchoring enzymes, and tag lengths merely by modifying appropriate parameters.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that certain changes and modifications
30 will be practiced. Therefore, the description and examples should not be construed as limiting the scope of the invention, which is delineated by the appended claims.

Table 1

Breast Cancer - Transcripts upregulated in metastatic breast tumor cells

| Sequence | Description | Accession | SEQ ID NO |
|-------------|--|-----------|-----------|
| GGTATGTTGT | | | 1 |
| ATGCTCCCTG | Human Mac-2 binding protein mRNA, complete cds. | L13210 | 2 |
| GTCTGGGGGA | Human lysophospholipase homolog (HU-K5) mRNA, comp | U67963 | 3 |
| GGTTGAAAAA | | | 4 |
| CGGATTATCC | H.sapiens BM28 mRNA. | X67334 | 5 |
| CTTCCTTGCC | Human radiated keratinocyte mRNA 266 (keratin-rela | X05803 | 6 |
| GTCATAGCTG | Homo sapiens (DCIS-1) mRNA fragment. | L27636 | 7 |
| CTTCAAGAGA | | | 8 |
| TGGACCCCCC | | | 9 |
| GTCTGCACCT | | | 10 |
| CTGTGCAGCA | Human spermidine synthase mRNA, complete cds. | M34338 | 11 |
| TGGATCAACC | H.sapiens mRNA for caveolin. | Z18951 | 12 |
| CTCCCTCCTC | Human thymidine kinase mRNA, complete cds. | K02581 | 13 |
| ATCGTGCGG | Homo sapiens hCPE-R mRNA for CPE-receptor, complet | AB0007 | 14 |
| AAAGAAAAAA | | | 15 |
| CCTGAAAAGC | | | 16 |
| TGTAGGTCAT | | | 17 |
| CCTGACGCTC | | | 18 |
| TGTTTCATCAT | | | 19 |
| TACGGTGGCG | H.sapiens mRNA for p cadherin. | X63629 | 20 |
| GCAGGAATTG | Human farnesyl pyrophosphate synthetase mRNA (hpt8 | M29863 | 21 |
| ACTTTTCAA | | | 22 |
| ATCCGTGCCC | Human calmodulin mRNA, complete cds. | J04046 | 23 |
| TTCTTATTTT | Human spliceosome associated protein (SAP 145) mRN | U41371 | 24 |
| CAGTCCGCTT | | | 25 |
| GTCACCCCCA | Homo sapiens intermediate conductance calcium-acti | AF0330 | 26 |
| GCACTGAATA | | | 27 |
| TTGCCCCCGT | H.sapiens mRNA for tyrosine kinase receptor. | X66029 | 28 |
| GGCAACAAAG | | | 29 |
| GCGGGGTGGA | | | 30 |
| GAGGGGAAAC | Human p66shc (SHC) mRNA, complete | U73377 | 31 |

| | | | |
|------------|--|--------|----|
| | cds. | | |
| CCCGCCCCCG | H.sapiens LU gene for Lutheran blood group glycopr | X83425 | 32 |
| GCTCAGGTCT | | | 33 |
| AATTGTCCGT | | | 34 |
| AAGGGCGCGG | Human lipocortin-III mRNA, complete cds. | M20560 | 35 |
| CCCTGGCAGG | | | 36 |
| TACTTCACTG | Homo sapiens clone Dt1P1b11 mRNA, CAG repeat regio | U92983 | 37 |
| GGCTCCCAAG | | | 38 |
| TTGGCGGGTC | | | 39 |
| ATCTGGGGCA | | | 40 |
| CCCCAGTGAG | | | 41 |
| CCTGTCATCC | | | 42 |
| CAAGGGTAAG | | | 43 |
| TTTAAAAAA | EGR3=EGR3 protein [human, HG 6.6, Zap33, Zap5a, Za | S40832 | 44 |
| TCAATAAAGA | H.sapiens QRSHs mRNA for glutaminyl-tRNA synthetas | X76013 | 45 |
| GCTCTCAGGG | Human polyhomeotic 2 homolog (HPH2) mRNA, complete | U89278 | 46 |
| CCTTGACCAA | | | 47 |
| CGGGGCGCGC | | | 48 |
| GAGTAGAGAA | | | 49 |
| CCCGGGAGCG | Homo sapiens carboxyl terminal LIM domain protein | U90878 | 50 |
| CAGCGCTGCA | Human CDC37 homolog mRNA, complete cds. | U63131 | 51 |
| GGATATGTGG | Human mRNA for early growth response protein 1 (hE | X52541 | 52 |
| TGCTTTCAA | | | 53 |
| GCCCAGCTCA | Human mRNA for 26S proteasome subunit p31, complet | D38047 | 54 |
| GATCTCTTGG | H.sapiens CaN19 mRNA sequence. | M87068 | 55 |
| GTTCGGGCCG | | | 56 |
| GGCAGGCACA | H.sapiens mRNA for phenylalkylamine binding protei | Z37986 | 57 |
| GGCCCTAGGC | | | 58 |
| TAGAAAGGCA | | | 59 |
| GGCAGGCGGG | Human ets domain protein ERF mRNA, complete cds. | U15655 | 60 |
| GGAGTGTGCT | | | 61 |
| TTCCGTTTCT | | | 62 |
| AAGCCCCTGG | | | 63 |
| ACCGGGGTGA | | | 64 |

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|------------|--|--------|----|
| ACTGACTCCA | | | 65 |
| CCGAAAAAGT | Human mRNA for RanBP1 (Ran-binding protein 1), com | D38076 | 66 |
| CCTGGACGCT | | | 67 |
| CTGAGGCGCT | Human thimet oligopeptidase (THOP1) mRNA, complete | U29366 | 68 |
| GCCCAGCGGC | | | 69 |
| CAGTGCGTTC | Human heart protein (FHL-2) mRNA, complete cds. | U29332 | 70 |
| CACACAATGT | | | 71 |
| CCCTGGTCCC | | | 72 |
| AAAACTTTTG | | | 73 |
| TGGGCCTTCC | | | 74 |
| ACCTCACTTA | | | 75 |
| TCCTGTAAAG | | | 76 |
| GGCTGATTTT | Human apobec-1 binding protein 1 mRNA, complete cd | U76713 | 77 |
| GGTCGGAAAA | | | 78 |
| CCACCACCCA | Human mRNA for calretinin. | X56667 | 79 |
| TGTTCTCCAT | Homo sapiens mRNA for OTK27, complete cds. | D50420 | 80 |
| GTTTATGATC | Homo sapiens mRNA for 5-aminoimidazole-4-carboxami | D89976 | 81 |
| TAAAAGACAA | | | 82 |
| AAGCTGTTCC | Human GP36b glycoprotein mRNA, complete cds. | U10362 | 83 |
| TGTCTGTGCC | | | 84 |
| AGCTGGGTTG | | | 85 |
| GCCCAGCAGG | | | 86 |
| ACTCTCCCGT | | | 87 |
| TCTGTTCTGG | Human ubiquitin conjugating enzyme mRNA, partial c | L22005 | 88 |
| TGCAATAGGG | | | 89 |
| AGCGGCCGCG | Human homolog of D. melanogaster flightless-I gene | U01184 | 90 |
| TCTCCTGGAC | | | 91 |
| TGGGATGCGC | | | 92 |
| TTAATATATG | | | 93 |
| ATTGACCGCT | | | 94 |
| GCCAACCTGC | | | 95 |
| TTTATAAGTT | | | 96 |
| CCGCGTCCCT | Human peroxisome proliferator activated receptor m | L07592 | 97 |
| TTTTTGATAA | Human HepG2 3' region cDNA, clone hmd2c11. | D16891 | 98 |
| TTTTTGATCA | H.sapiens mRNA for beta-catenin. | X87838 | 99 |

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|-------------|--|--------|-----|
| CTTATGATCA | | | 100 |
| ACCTTCACCA | | | 101 |
| TCTGCAATGA | | | 102 |
| CCCCCCTTCT | | | 103 |
| CAGCCTTGCG | | | 104 |
| GTGTCGCGTG | | | 105 |
| CATTCAGAG | | | 106 |
| TCAATCAAGA | 14.3.3 eta chain=brain-specific tyrosine and trypt | S80794 | 107 |
| CCCTGGAGAC | | | 108 |
| TTTTAAAAAT | Homo sapiens catechol-O-methyltransferase (COMT) m | M65213 | 109 |
| TGAATCTGGG | Human set gene, complete cds. | M93651 | 110 |
| ATTCTGCCTC | | | 111 |
| GGAAGGCGGC | | | 112 |
| CGGATGATTG | | | 113 |
| CTGAGGGTCG | | | 114 |
| GGTGAGGTGG | | | 115 |
| GTGTGTTTGT | Human transforming growth factor-beta induced gene | M77349 | 116 |
| CCCCGTATGG | | | 117 |
| CGCGTGACACA | Homo sapiens TTF-I interacting peptide 21 mRNA, pa | AF0005 | 118 |
| AAGAAGGCAC | | | 119 |
| AACGAGTACA | | | 120 |
| GATAGTTGTG | | | 121 |
| ACCAGCTCCC | | | 122 |
| GAACGTCTCT | | | 123 |
| CAGGGCGGTG | | | 124 |
| AAAGATGATG | | | 125 |
| TAACTGTGT | | | 126 |
| ACACAGCCAA | | | 127 |
| ACAGCGTCTG | | | 128 |
| GAATCTGGAG | | | 129 |
| TTTGAGACCT | | | 130 |
| ATGTGAAGAA | | | 131 |
| GTGTACCGGA | Human cytohesin-2 mRNA, complete cds. | U70728 | 132 |
| ATGCCTTGGG | | | 133 |
| ATCTGTCCCT | | | 134 |
| GGGGGCTGCT | | | 135 |
| CTCCTTAAGA | | | 136 |
| GCCGAGCCGC | | | 137 |
| ATGGTGGGCA | Human zinc finger protein (ZNF139) mRNA, partial c | U09848 | 138 |
| TCTTCTAAAA | | | 139 |

| | | | |
|------------|--|--------|-----|
| TCATAACTGT | Human mRNA for flavoprotein subunit of complex II, | D30648 | 140 |
| TGGATGCTGT | | | 141 |
| AAAACTGCCT | | | 142 |
| TCCTTTGTGC | | | 143 |
| GCCCTCCGGC | | | 144 |
| GATGCGAGGA | Human semaphorin III family homolog mRNA, complete | U38276 | 145 |
| CAGAGATGAA | | | 146 |
| CCACACCTCT | | | 147 |
| GACGCAGAAG | | | 148 |
| AGCGCCTTCC | | | 149 |
| ACGCTGCTGC | | | 150 |
| CAAGGGCCAA | Human RalGDS-like 2 (RGL2) mRNA, partial cds. | U68142 | 151 |
| CTGCGGAAGA | | | 152 |
| CCTGGAATGA | | | 153 |
| CCTGAAATCC | | | 154 |
| CCTCGGAGAT | Homo sapiens 9G8 splicing factor mRNA, complete cd | L22253 | 155 |
| CAGTTAGGGA | | | 156 |
| CACGGGTGTC | | | 157 |
| CAACTCAAAC | Human mRNA for tyrosine kinase, complete cds. | D31661 | 158 |
| ATTTGGCTTT | | | 159 |
| ATTCTGCTTT | | | 160 |
| ATGGCAGAGA | | | 161 |
| ATGAGGCCGG | | | 162 |
| CTTGACACAC | | | 163 |
| ACGTCTCTAT | | | 164 |
| GACCCTGACT | | | 165 |
| AATACTTTTG | | | 166 |
| AAGGTGGAGA | | | 167 |
| AACTCTTCAC | Human beta adaptin mRNA, complete cds. | M34175 | 168 |
| AACCACTGTG | | | 169 |
| TTTTGCTTTT | | | 170 |
| TTTCTCGGTG | | | 171 |
| TTGAACTGGC | | | 172 |
| TTAGTCAGGC | Human transmembrane 4 superfamily protein (SAS) mR | U01160 | 173 |
| TTACCTTTTT | Human beta-galactosidase (GLB1) mRNA, complete cds | M34423 | 174 |
| TTACCTTACC | | | 175 |
| TGTTCAAGAC | | | 176 |
| TGTCTGCCTG | | | 177 |

| | | | |
|------------|--|--------|-----|
| TGTCCCCTCA | Human rac protein kinase alpha mRNA, complete cds. | M63167 | 178 |
| ATCGTGCCAC | | | 179 |
| GTGTCCGGCG | Homo sapiens mRNA for U3 snoRNP associated 55 kDa | AJ0013 | 180 |
| TTTCCAGCAT | | | 181 |
| TTAATAAAAT | Human GST1-Hs mRNA for GTP-binding protein. | X17644 | 182 |
| TGCGCCTTTA | | | 183 |
| TGATGTTGGA | | | 184 |
| TGATGCAGCC | Human SNARE protein Ykt6 (YKT6) mRNA, complete cds | U95735 | 185 |
| TGAATGTCAA | | | 186 |
| TCTGTAAGGG | Human mRNA for KIAA0129 gene, complete cds. | D50919 | 187 |
| TCTGCAAATT | | | 188 |
| TCTCTACTAA | Human clone 3, Alu repeat sequence. | U02060 | 189 |
| TCGCCCACTC | | | 190 |
| TCCTGCTGAT | Human mRNA for KIAA0079 gene, complete cds. | D38555 | 191 |
| TAGGAAAGTA | Human tissue factor gene, complete cds, with a Alu | M27436 | 192 |
| CTTACAACCG | | | 193 |
| GTTTTTAAAT | Homo sapiens putative oncogene protein mRNA, parti | AF0268 | 194 |
| TGGAAGGACC | | | 195 |
| GTATTIGCAA | | | 196 |
| GTAGAAAAGA | | | 197 |
| GGGGAGCTCG | | | 198 |
| GCTGCTGCCT | | | 199 |
| GCTCCCGGAC | | | 200 |
| GCTATCTCAG | | | 201 |
| GCGGCGGCGA | | | 202 |
| GCCTGGGACC | | | 203 |
| GCAAGCCCAA | | | 204 |
| GATGGGGTTC | | | 205 |
| GATACACTGG | | | 206 |
| GAGAATCTGA | | | 207 |
| GACTCCACAT | | | 208 |
| TAACCAAACA | | | 209 |
| CCCCAAGACC | | | 210 |
| GAGAGTGTAC | | | 211 |
| GACCACACCG | | | 212 |
| GACACCAACT | Homo sapiens deubiquitinating enzyme UnpEL (UNP) m | AF0173 | 213 |
| GAAGGAGATG | | | 214 |

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|------------|--|--------|-----|
| GAAGATTAAT | TCR alpha=T-cell receptor alpha chain {VDJ region, | S69283 | 215 |
| CTTTGCTTTT | H.sapiens mRNA for PHAPI2b protein. | Y07570 | 216 |
| CTGTCTGTGG | | | 217 |
| CTGGGGGTCT | | | 218 |
| CTCTGATGCA | H.sapiens mRNA for DNA polymerase gamma, mitochond | X98093 | 219 |
| CTCTACAGTG | Homo sapiens mRNA for vacuolar proton-ATPase subun | Y15286 | 220 |
| CGCCTGTAGT | | | 221 |
| CCTGGAGGGG | | | 222 |
| TGTAAGAAAA | Human mRNA for HsMcm6, complete cds. | D84557 | 223 |
| CCCCTGCTAG | | | 224 |
| GCACGTGTCT | | | 225 |
| CCCCAAGACA | | | 226 |
| CCCAGCTAAT | Human 15-lipoxygenase mRNA, complete cds. | M23892 | 227 |
| TCTCAGTGTC | | | 228 |
| CAGCGCACAG | | | 229 |
| CAAACCTTTA | | | 230 |
| CAAACCTTGT | | | 231 |
| ATTTTCAAAA | H.sapiens mRNA for gamma-adaptin. | Y12226 | 232 |
| ATCTTGGCCT | | | 233 |
| ATCTCTGGAG | | | 234 |
| AGTTGAAATT | | | 235 |
| AGACCTCCTT | | | 236 |
| AGACAAGCTG | Human splicing factor SRp40-3 (SRp40) mRNA, comple | U30827 | 237 |
| ACTGTTTGGC | | | 238 |
| CCGTCTTTCC | | | 239 |
| GGTTCTGTAG | | | 240 |
| ACTCGTGCTC | | | 241 |
| TGCCAAACGG | | | 242 |
| TGAAGAAAGG | Human integral membrane protein CII-3 mRNA, nuclea | U57877 | 243 |
| TCTGGACCGG | | | 244 |
| TCTGCTAAAA | | | 245 |
| TCTCAGTGTT | | | 246 |
| TCCGCCGCCC | | | 247 |
| TCAGACCCAG | | | 248 |
| TATCTGCTGA | | | 249 |
| TACGTTGCAG | | | 250 |
| GTTGTAAAAT | | | 251 |
| GTGGAATAAA | latent transforming growth factor-beta-binding pro | S82451 | 252 |

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|------------|--|--------|-----|
| GTCCTGGAGG | | | 253 |
| GAGGCGCTGG | Homo sapiens bcl-xL/bcl-2 associated death promote | AF0315 | 254 |
| GCTGAGCTGG | Human alpha-N-acetylglucosaminidase (NAGLU) mRNA, | U43573 | 255 |
| TGGTTGCGAC | Human branched chain aminotransferase precursor (B | U68418 | 256 |
| GCCAGCGTCA | Homo sapiens spindle pole body protein spc97 homol | AF0423 | 257 |
| GCCCCAGAAT | | | 258 |
| GCCGAGCTGG | | | 259 |
| GCCTGAGGGG | | | 260 |
| GTCCGAGTGC | | | 261 |
| GCTCACCTGT | | | 262 |
| GGTTTGAAG | | | 263 |
| GGAAATGTCA | Human collagenase type IV mRNA, 3' end. | J03210 | 264 |
| GGACTTTGAG | | | 265 |
| GGAGTAGGAA | | | 266 |
| GGGGCACTTG | H.sapiens mRNA for nicein B2 chain. | X73902 | 267 |
| GGTGCAAAAG | | | 268 |
| GATGTCTTGT | | | 269 |
| GCTATGCTCC | | | 270 |
| GTCACTGCCT | | | 271 |
| GACTCGCCCA | H.sapiens P1-Cdc46 mRNA. | X74795 | 272 |
| CCTGTCCAGC | | | 273 |
| CACTACTCAC | | | 274 |
| TTGAAGTGCG | | | 275 |
| TGCTGTGTGC | | | 276 |
| TAGTATTTTC | | | 277 |
| GCCCCACAGC | | | 278 |
| AGAGACAAGT | | | 279 |
| GGCCGCGTTC | Human ribosomal protein S17 mRNA, complete cds. | M13932 | 280 |
| TGGAAAATTT | | | 281 |
| AATGTGATTT | Human prolylcarboxypeptidase mRNA, complete cds. | L13977 | 282 |
| TGCCTGTGAA | | | 283 |
| TGCAGGTACT | Human mRNA for LIMK-2, complete cds. | D45906 | 284 |
| ACATTCTTTT | H.sapiens NMB mRNA. | X76534 | 285 |
| GCCTGCCTGA | H.sapiens mRNA for hair keratin, hHb3. | X99141 | 286 |
| TGAGTTGGCC | | | 287 |
| TGGGTCTGAA | | | 288 |
| TGAAACTTTT | | | 289 |
| AATAAAAGAC | | | 290 |

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| TGGAATGAGC | Human sarcomeric mitochondrial creatine kinase (Mt | J05401 | 291 |
| ACGCCCCACCT | | | 292 |
| TCCAAGTTCC | | | 293 |
| TCCAAAGCAT | | | 294 |
| TCAACTGGTT | H.sapiens mRNA for phosphoenolpyruvate carboxykina | X92720 | 295 |
| TATTTATTGA | | | 296 |
| ACGGTCCAGG | Homo sapiens cytidine deaminase (CDA) mRNA, comple | L27943 | 297 |
| TGAAGGTGGA | Human mRNA for KIAA0330 gene, partial cds. | AB0023 | 298 |
| TTGGTTTTGT | | | 299 |
| AAAAACCATA | Homo sapiens transcription factor TFIIA small subu | U21242 | 300 |
| TTTTGATGAG | | | 301 |
| TTTGCTTTTG | | | 302 |
| AACGGGCCCGG | | | 303 |
| TTTGCTCTCC | Human vinculin mRNA, complete cds. | M33308 | 304 |
| TGATTTCACT | Human autonomously replicating sequence (ARS) mRNA | L08441 | 305 |
| TTTATTTCTA | | | 306 |
| AATCAAACAC | Homo sapiens DNA polymerase alpha mRNA, complete c | L24559 | 307 |
| AAGGAAACGT | | | 308 |
| TGGAGAATGT | | | 309 |
| TTGCTGGAGA | | | 310 |
| TGTTTATCCT | Human endozepine (putative ligand of benzodiazepin | M15887 | 311 |
| TGTACTACTT | | | 312 |
| TAGCAGCTGG | | | 313 |
| AAGGTAATAT | Homo sapiens microsomal glutathione S-transferase | U77604 | 314 |
| TATATCAGTG | | | 315 |
| TGGCCAATAA | | | 316 |
| AACCAAAAAA | | | 317 |
| TTTACAGACC | | | 318 |
| GAGAAGGGCA | | | 319 |
| TATGATTACC | Human mRNA for platelet activating factor acetylhy | D63391 | 320 |
| GCTGCTGGCA | | | 321 |
| GCTAATAGTA | | | 322 |
| GCCTCTTGAA | hCDC10=CDC10 homolog [human, fetal lung, mRNA, 231 | S72008 | 323 |
| GCCATCCAGA | | | 324 |
| GCCAGACCCC | | | 325 |

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| GCACTCAATA | | | 326 |
| GATTTGAAAT | | | 327 |
| GATGAGGAAC | | | 328 |
| GGACTTAGAA | | | 329 |
| GAGCTTTTGA | | | 330 |
| GGATCCCAAC | | | 331 |
| GAGAAGACTT | H.sapiens mRNA for prolyl oligopeptidase. | X74496 | 332 |
| GACGTCTTAA | Human mRNA for proteasome subunit HC9. | D00763 | 333 |
| GACACGTGAC | | | 334 |
| GAAGTGGAAG | | | 335 |
| GAACATAGCC | | | 336 |
| CTTGATTAAA | | | 337 |
| CTGTGTAAGC | Human L-isoaspartyl/D-aspartyl protein carboxyl me | M93009 | 338 |
| CTGATGGCAG | | | 339 |
| CTGAGACACC | | | 340 |
| CGTGCCGCCT | | | 341 |
| GAGTATCTCA | | | 342 |
| GTGCAGTACC | | | 343 |
| TAGACTGGCA | | | 344 |
| TACAAAACCA | | | 345 |
| TAACGAACAA | | | 346 |
| GGGAAGCAGA | | | 347 |
| TAACAGGAAA | | | 348 |
| CGAGGGGGCCA | | | 349 |
| GTTTGTGATG | | | 350 |
| GTTGGTCCCT | | | 351 |
| GTGTCCTCCT | Human Golgi membrane sialoglycoprotein MG160 (GLG1 | U64791 | 352 |
| GCTTCTGCAT | | | 353 |
| GTGGCACCAC | | | 354 |
| AGCGTGGCTC | | | 355 |
| GTGATTCATT | | | 356 |
| GTCTCACGTG | | | 357 |
| GGTTGGCAGG | | | 358 |
| GGTACTCGAT | | | 359 |
| GGGCCGCTCA | Homo sapiens mRNA for KIAA0602 protein, partial cd | AB0111 | 360 |
| GGGCCCCGCA | Human mRNA for KIAA0123 gene, partial cds. | D21064 | 361 |
| GGGCAGAATT | Human mRNA for KIAA0370 gene, partial cds. | AB0023 | 362 |
| GGGAGTGCGC | | | 363 |
| GGCTCAGCAG | | | 364 |

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| GGCGCCAGCG | | | 365 |
| GTGTCCATCT | Homo sapiens tumor-suppressing subchromosomal tran | AF0199 | 366 |
| TCAGTGGTAG | | | 367 |
| AGCAGCTCAC | | | 368 |
| TATAAATTTT | | | 369 |
| GCAGGCCTGC | | | 370 |
| GCAGAGAAGC | Human myogenic repressor I-mf (MDFI) mRNA, complet | U78313 | 371 |
| GCAAATGCCG | Homo sapiens U4/U6 small nuclear ribonucleoprotein | AF0163 | 372 |
| GATGTTGCTC | | | 373 |
| GATGTTAGTA | | | 374 |
| GAGTCTGAGG | Human mRNA for hU1-70K small nuclear RNP protein (| X06816 | 375 |
| GAGGCAGCTG | Human GTP-binding protein (HSR1) mRNA, complete cd | L25665 | 376 |
| GCCCACAAGT | | | 377 |
| GAGCAGGAGC | Homo sapiens mRNA for KIAA0600 protein, partial cd | AB0111 | 378 |
| TACAGCGAGC | | | 379 |
| GAGAGACACG | | | 380 |
| TCCCAGAGAC | Human mRNA for beta-1,4-galactosyltransferase, com | D29805 | 381 |
| GACACTGAAA | | | 382 |
| TCGCGGGCCT | Human clone 23882 mRNA, complete cds. | U79303 | 383 |
| GAAGTGCCTC | Homo sapiens FLICE-like inhibitory protein short f | U97075 | 384 |
| GAAAGATTGG | | | 385 |
| CTTTTCACTT | | | 386 |
| CTTCCCACTC | | | 387 |
| CTTCAGAAAT | | | 388 |
| GAGCGGGATC | Human alternative splicing factor mRNA, complete c | M72709 | 389 |
| GTGGCGTATG | | | 390 |
| GGTGGTCAGA | transcription factor E2F like protein [human, mRNA | S49592 | 391 |
| GGTGCAGAGC | | | 392 |
| GTATACAACA | | | 393 |
| GTCATTTGGA | | | 394 |
| GGCTGTAAGT | | | 395 |
| GTGAAGTTAC | | | 396 |
| GTGAGAAGTG | | | 397 |
| GTGAGCCACA | | | 398 |
| GTGATGTCTG | | | 399 |

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| TACGATGAGT | Human low molecular mass GTP-binding protein (ral) | M29893 | 400 |
| GGAGTCCCTT | | | 401 |
| CTGTACTAGG | | | 402 |
| GGAGCACACA | | | 403 |
| GTGTTCTGAC | | | 404 |
| GGACGGAAGT | | | 405 |
| GCTTGTTAAG | Homo sapiens S-adenosyl homocysteine hydrolase hom | U82761 | 406 |
| GTTTCCACCG | | | 407 |
| GCTGCCAGCA | | | 408 |
| GCTCAACATC | | | 409 |
| GCGGGGTGAC | Human regulator of nonsense transcript stability (| U65533 | 410 |
| TAATCAGGAG | | | 411 |
| GTGCTCCTAG | | | 412 |
| ATCGTGGCTG | | | 413 |
| CCCTGCTTCC | | | 414 |
| TTTTGGGCAG | | | 415 |
| CCCCTTATTT | | | 416 |
| TTTTGTACCA | | | 417 |
| TTTTTACTCA | | | 418 |
| CCAGTGGCTC | Homo sapiens myo-inositol monophosphatase 2 mRNA, | AF0143 | 419 |
| CAGTGTATAT | | | 420 |
| CAGAAATGAA | Human ubiquitin-homology domain protein PIC1 mRNA, | U61397 | 421 |
| CACTGTGTTG | | | 422 |
| TCTGCAAGCA | | | 423 |
| CAACTATCCG | | | 424 |
| TTGGCTTTTC | | | 425 |
| ATCCATTCTG | | | 426 |
| ATCCAGCAGA | | | 427 |
| ATCATCCAGG | | | 428 |
| ATCAGTGTGA | acidic calponin [human, kidney, mRNA, 1607 nt]. | S80562 | 429 |
| AGGTCAAGAG | | | 430 |
| AGGAAGGGGT | | | 431 |
| TCCAAATCGA | Human vimentin (HuVim3) mRNA, 3' end. | M25246 | 432 |
| AGCCAGCCTA | | | 433 |
| CGGCACATCC | Human galactokinase (galK) mRNA, complete cds. | U26401 | 434 |
| CACCACGGTG | | | 435 |
| CTACCCAACA | | | 436 |
| AGCACAGGGA | Human PML-3B mRNA, complete CDS. | M80185 | 437 |

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| CTGGCCATCG | | | 438 |
| CTGCCTTCTT | Human protein phosphatase-1 gamma 1 mRNA, partial | L07395 | 439 |
| CTGCAGGACC | | | 440 |
| TGCAGCCGCT | | | 441 |
| TGCTGAGGAA | | | 442 |
| TGCTGGTGTG | Human mRNA, clone HH109 (screened by the monoclonal) | D23673 | 443 |
| TGGAAAGCTT | Homo sapiens chick ovalbumin upstream promoter tra | M62760 | 444 |
| CTCCAATAAA | | | 445 |
| TTTTACCACT | H.sapiens mRNA for lcln protein. | X91788 | 446 |
| CTACGTGATG | Nrf2=NF-E2-like basic leucine zipper transcription | S74017 | 447 |
| CCCTTGTGAC | | | 448 |
| CGTTTTCTGA | Homo sapiens protein tyrosine phosphatase (PRL-1) | L39000 | 449 |
| CGGGTAGTAT | Human acid alpha-glucosidase (GAA) mRNA, complete | M34424 | 450 |
| TTAGCCAGGA | Human LLGL mRNA, complete cds. | D50550 | 451 |
| CGCCCCACA | | | 452 |
| TCGGAGCTGC | Human ras inhibitor mRNA, 3' end. | M37192 | 453 |
| CCTGGGTCCT | | | 454 |
| TTGCCGCTGC | | | 455 |
| TTGGAGGAGT | | | 456 |
| CCTCCCCGAA | | | 457 |
| CTTAATGGTG | | | 458 |
| CTAGTCACTT | | | 459 |
| ACCCTTTAAC | H.sapiens HLA-E gene. | X56841 | 460 |
| AACCAGGTGT | Human mitochondrial RNA polymerase mRNA, nuclear g | U75370 | 461 |
| AAATGCCCTC | Human translational initiation factor (eIF-2), alp | J02645 | 462 |
| GGCGTCCTGG | | | 463 |
| TCTGTTTCCA | Human tyrosine kinase (HTK) mRNA, complete cds. | U07695 | 464 |
| AAGCTGTGTC | | | 465 |
| CAGCTGGGGC | Human polypyrimidine tract-binding (PTB) mRNA for | X60648 | 466 |
| AAGTATTGTG | Homo sapiens phosphatidylinositol 4-kinase 230 (pi | AF0128 | 467 |
| ATGTCATCAA | Human clathrin assembly protein 50 (AP50) mRNA, co | U36188 | 468 |
| ACCAAAGCCC | | | 469 |
| AGCCTTTCCG | | | 470 |
| ACCCTTGGGC | | | 471 |

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| ATGAACCGCA | | | 472 |
| ACCTCTCTAA | | | 473 |
| ACCTCTGGCT | Human homeobox protein (PHOX1) mRNA, 3' end. | M95929 | 474 |
| ATCTCAAAGA | | | 475 |
| ACCTGCTTAA | nucleoprotein interactor 1=SRP1 homolog [human, ce | S75295 | 476 |
| AAAAGAAACT | Human mRNA for polyA binding protein. | Y00345 | 477 |
| AGAAATCACT | Human 3-hydroxyacyl-CoA dehydrogenase mRNA, partia | AF0019 | 478 |
| TGGTCCACGG | | | 479 |
| GAGGGACCCA | | | 480 |
| AAGCAAGTCA | | | 481 |
| ACCAGCGTGT | Human mRNA for KIAA0150 gene, partial cds. | D63484 | 482 |
| TTAAAGGCCG | Human MRL3 mRNA for ribosomal protein L3 homologue | X06323 | 483 |
| GGCGTGAACC | Human cyclin protein gene, complete cds. | M15796 | 484 |
| TAGTAGATGC | | | 485 |
| GCCAAGATGC | | | 486 |
| TAAGTTCCTT | | | 487 |
| CCAGCTGCCA | Human ubiquitin-activating enzyme E1 (UBE1) mRNA, | M58028 | 488 |
| GCCCCGCCCT | | | 489 |
| TATCTGTCTA | | | 490 |
| TACCCACCT | | | 491 |
| TCAGTGAACG | Homo sapiens p87/89 gene, complete cds. | L42572 | 492 |
| CCTTTGTAAG | | | 493 |
| CAGCTCCGCT | Human deoxyuridine triphosphate nucleotidohydrolas | U90223 | 494 |
| AAACTGACAG | | | 495 |
| GACCCCAAGG | Human cyclin mRNA. | M74092 | 496 |
| TCGCCGGGCG | Human hindlimb expressed homeobox protein backfoot | U70370 | 497 |
| GTGAAACACC | | | 498 |
| GTAGCATAAA | | | 499 |
| TCCTTGCTTC | | | 500 |
| GTAGACTCAC | Human HLA-B-associated transcript 2 (BAT2) mRNA, c | M33509 | 501 |
| GCCCAGCCCT | Homo sapiens cDNA mapping to 22q13. | AL0216 | 502 |
| GGTTAAGAGC | Human Lewis blood group locus mRNA for | X53578 | 503 |
| AAAACAATGG | | | 504 |

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| GACTAGTGCG | | | 505 |
| TGCGGAGGCC | Homo sapiens mRNA for p27, complete cds. | AB0017 | 506 |
| CCAAAATTAG | | | 507 |
| ACCATCCTGC | Homo sapiens mRNA for cadherin-6, complete cds. | D31784 | 508 |
| AGAGCAAGTA | | | 509 |
| ACTGCCTCTT | | | 510 |
| CACTCCAGCC | | | 511 |
| CAGACCCTGC | | | 512 |
| ACACACGCAA | | | 513 |
| CAGCCTTGGA | | | 514 |
| GGAACAAACA | Homo sapiens CD24 signal transducer mRNA, complete | L33930 | 515 |
| AAAGGGGGCA | | | 516 |
| AGGCTGTCCA | | | 517 |
| GGGGGTAAC | TLS=translocated in liposarcoma [human, mRNA, 1824 | S62140 | 518 |
| CACGCGCTCA | Human mRNA for RPB5 (XAP4), complete cds. | D38251 | 519 |
| CCAACAATA | | | 520 |
| CCAAGAAAGA | Homo sapiens polyadenylate binding protein mRNA, c | U75686 | 521 |
| CCCATTCTC | | | 522 |
| TGGTTTTTGG | | | 523 |
| ACCTGGGGAG | Homo sapiens lysophosphatidic acid acyltransferase | AF0002 | 524 |
| GAGCACATCA | | | 525 |
| TCCGAGACTG | | | 526 |
| GTGCCTGAGA | Human lamin A mRNA, 3'end. | M13452 | 527 |
| TACTGGAAGT | | | 528 |
| CCTGTCAATG | | | 529 |
| CATTGAGCTC | | | 530 |
| TCTGCTAAAG | | | 531 |
| CGCTGTTTTT | | | 532 |
| AGGGATCCTA | | | 533 |
| AGTGAAATAA | | | 534 |
| AGTGTCTGTG | H.sapiens CYR61 mRNA. | Y11307 | 535 |
| ATCACGCCCC | | | 536 |
| ATCCACCCGC | general transcription factor IIE 56 kda subunit [h | S67859 | 537 |
| ATCTCCAGGT | | | 538 |
| ATCTTGAAAG | H.sapiens NAP (nucleosome assembly protein) mRNA, | M86667 | 539 |
| AGCCTGTTGC | | | 540 |
| AAACTCGGGT | | | 541 |

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| CCACACACCG | | | 542 |
| AAGATTGGTG | Human CD9 antigen mRNA, complete cds. | M38690 | 543 |
| CAAAGGAAGC | H.sapiens (TL15) mRNA from (DU145) cell line. | X75689 | 544 |
| CGGCTCAAGT | | | 545 |
| CGTGCTGGCC | | | 546 |
| CCCTTAAGTT | | | 547 |
| CCCAGGGCTC | | | 548 |
| ATGGTGCTGA | Human SREBP-1 mRNA, complete cds. | U00968 | 549 |
| TGATTTTCTT | SC1=putative trans-acting factor involved in cell | S53374 | 550 |
| TCTTCGTCCT | | | 551 |
| TCTTTGATCT | | | 552 |
| TCTGCCTGTC | | | 553 |
| TGAAGAATGG | Homo sapiens trinucleotide repeat 5-d(CGG)n-3ds bi | AJ0002 | 554 |
| GCTGAAGATG | | | 555 |
| TGATGGGCAT | | | 556 |
| GCTGAAACTT | | | 557 |
| TTGCTTAGTT | Human mRNA for KIAA0326 gene, partial cds. | AB0023 | 558 |
| TGTGAGCCTC | H.sapiens mRNA for cyclin F. | Z36714 | 559 |
| GCGGCCCTGG | | | 560 |
| TTCTCCAAA | | | 561 |
| TTCTCAAGGC | | | 562 |
| TTCTCTCCAC | | | 563 |
| TTCTTTTCT | | | 564 |
| TTCAATTTCA | Homo sapiens amplexin (EMS1) mRNA, complete cds. | M98343 | 565 |
| GCGACTTTTT | | | 566 |
| TTATGGATCT | | | 567 |
| GCGAAGGCTC | | | 568 |
| GCCTTTCTAA | Homo sapiens ribosomal protein S6 kinase 2 (RPS6KA | L07597 | 569 |
| TTGGCAGTAT | Homo sapiens epsilon-sarcoglycan (ESG) mRNA, compl | AF0363 | 570 |
| TTGGCCCAGG | | | 571 |
| GCCTAGTACT | | | 572 |
| TTGTGAGAAT | | | 573 |
| TTTGAGTTTT | | | 574 |
| TTGCAAAGGG | | | 575 |
| GCTAAACAGG | | | 576 |
| GCTCCAGCTA | | | 577 |
| TGGAAATAAA | | | 578 |

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| TGGCAAGATG | | | 579 |
| TGGCTTGCTC | | | 580 |
| TGGTGGAGGC | | | 581 |
| TGGTTTGCAC | | | 582 |
| GCGGTGGCGG | | | 583 |
| GCTACTATTA | | | 584 |
| GCTCTGAAGG | | | 585 |
| TGTATGTCGC | | | 586 |
| TGTGGGGCTC | H.sapiens mRNA for histidyl-tRNA synthetase. | Z11518 | 587 |
| TGTTCCACTC | | | 588 |
| TGTTTATAGA | | | 589 |
| GCGTGACTTC | | | 590 |
| TTAAAGATTT | Homo sapiens mRNA for alpha-tropomyosin (3' end). | AJ0001 | 591 |
| TTAGCAGTTG | | | 592 |
| TGTATGCCGT | | | 593 |
| GGCGTTGTCT | | | 594 |
| GCTTTTATAC | | | 595 |
| GGACCAGGCT | | | 596 |
| GTTGGGTCAG | H.sapiens mRNA for TIM17 preprotein translocase. | X97544 | 597 |
| GTTCTAAACC | | | 598 |
| GGAGGCGGAG | | | 599 |
| GTTCCAGTGC | | | 600 |
| GGAGTTGTCC | | | 601 |
| GGATCTCCCA | | | 602 |
| GGCATAGGCT | | | 603 |
| GGCCCCCCTC | Human mRNA for KIAA0295 gene, partial cds. | AB0022 | 604 |
| GTGGATGTAC | | | 605 |
| GGCCCCCTAA | | | 606 |
| GGCCTATGAG | | | 607 |
| TATGGGTTCC | | | 608 |
| GTGAAACTCT | | | 609 |
| GGGGCAGCCG | | | 610 |
| GGGCTGCTCT | | | 611 |
| GTA CTGTATG | Homo sapiens importin beta subunit mRNA, complete | L38951 | 612 |
| GGGCGATACA | Homo sapiens mRNA for PCDH7 (BH-Pcdh)a, complete c | AB0067 | 613 |
| GGGCCCTTGG | | | 614 |
| GTGCCACCAG | | | 615 |
| GTCTGGGGGC | | | 616 |
| GGCGACGAGG | | | 617 |
| GTGAAATCCT | Homo sapiens mRNA for putative lipoic | AJ2241 | 618 |

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| | acid synthet | | |
| GGCTTTGATT | H.sapiens subunit of coatomer complex. | X70476 | 619 |
| GGCTGCCTGC | | | 620 |
| GTGACGCCCC | | | 621 |
| GGCTCTTCTG | | | 622 |
| TAAGTGTGGT | | | 623 |
| GTCTCCCGGC | | | 624 |
| TCCAGACAGC | Human Hpast (HPAST) mRNA, complete cds. | AF0014 | 625 |
| GCTTCGTTAC | | | 626 |
| TCACAAACTG | | | 627 |
| TCACAATACA | Human cyclophilin-40 mRNA, complete cds. | L11667 | 628 |
| TCACGCTGCT | | | 629 |
| TCAGGGCATT | | | 630 |
| TATTCAATTA | | | 631 |
| TCATCTTTGT | | | 632 |
| GCCCTGGAGC | | | 633 |
| TCCGTGTGTC | | | 634 |
| TCGGGAGCTG | | | 635 |
| TCGGGTGTGG | | | 636 |
| TCGGTTACAA | | | 637 |
| TCTACAAAAA | | | 638 |
| TCTGCAAAAA | | | 639 |
| TCATATGTGT | | | 640 |
| TACCTTTATT | Human serine kinase mRNA, complete cds. | U09564 | 641 |
| TCTGCAAAGG | Homo sapiens for mRNA encoding HMG2B. | Z17240 | 642 |
| GCTGTATAAT | | | 643 |
| TAATTAAGTC | | | 644 |
| TAATTTTCT | Homo sapiens clone 23705 mRNA sequence. | AF0353 | 645 |
| TACAGCCACT | | | 646 |
| TATTGTGTGT | Human mRNA for mitochondrial 75 kDa iron sulphur p | X61100 | 647 |
| TACCCCCGAG | | | 648 |
| GCTTCCCCAC | T3 receptor-associating cofactor-1 [human, fetal I | S83390 | 649 |
| GCTGATCTAC | Human casein kinase I delta mRNA, complete cds. | U29171 | 650 |
| TATAGTGGCT | | | 651 |
| TATGAACTGA | Human poly(ADP-ribose) polymerase mRNA, complete c | M32721 | 652 |
| TATGACCACA | | | 653 |

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| AAGTGCATTT | | | 654 |
| TATGGACCTG | | | 655 |
| GCTGGGTAAC | | | 656 |
| CAAGGAGATC | | | 657 |
| AAGGTGGCCA | Homo sapiens mRNA for KIAA0540 protein, partial cd | AB0111 | 658 |
| CTTTACTGTG | | | 659 |
| CAACCCACGC | | | 660 |
| CTTGTGTTAT | | | 661 |
| CTTGTGAAGT | | | 662 |
| CTTGAATTGC | | | 663 |
| CTTTGCACTC | Human transcription elongation factor (SII) mRNA, | M81601 | 664 |
| CTGGTGGCAT | | | 665 |
| CTTTTCCTGA | H.sapiens mRNA for TRAMP protein. | X63679 | 666 |
| CTGGTGATGG | | | 667 |
| CAATGGAGCT | | | 668 |
| CTGGGATCAT | | | 669 |
| CTGGCAGGCC | | | 670 |
| CACACTACTA | | | 671 |
| CACCACGGGC | | | 672 |
| CTGTGACACA | Homo sapiens chaperonin containing t-complex polyp | AF0262 | 673 |
| ATTTCAAAG | | | 674 |
| ATGGATGCAC | | | 675 |
| ATGGCCTCCT | Human syntaxin mRNA, complete cds. | U07158 | 676 |
| ATGTAGAATG | | | 677 |
| ATGTCATCTG | | | 678 |
| GAAGTTGCCT | | | 679 |
| ATGTTTGAAG | | | 680 |
| CTTCCCTTG | | | 681 |
| ATTGTCAGGG | | | 682 |
| CTGAACCTGA | Human CD39L1 mRNA, complete cds. | U91510 | 683 |
| ATTCTACCT | | | 684 |
| CAAACCTCCG | | | 685 |
| GAAGAGGATG | | | 686 |
| GAACGTCTTA | H.sapiens son-b mRNA. | X63751 | 687 |
| GAACCTGGAC | | | 688 |
| CTTTTTTTTG | | | 689 |
| ATTGAGCCAC | | | 690 |
| CCCTCCAGCT | | | 691 |
| CCACCGCACT | | | 692 |
| CCAGCGCCAA | | | 693 |
| CCTTTCAAAA | | | 694 |
| CCCAAGTAGC | | | 695 |
| CCCGCATTAG | | | 696 |

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| CCTTACCCAG | | | 697 |
| CACCCTGTAC | Human placental equilibrative nucleoside transport | U81375 | 698 |
| CCCGTCCAAG | | | 699 |
| CATTGTGCAC | | | 700 |
| CCCTGACCAA | | | 701 |
| CCGACCACAA | | | 702 |
| CCGTTCCAAG | | | 703 |
| CCTCTCCCAC | | | 704 |
| CCTACCACCA | | | 705 |
| CCTCCCCCTC | | | 706 |
| CCCGTAGCCC | | | 707 |
| CGGCTGACAG | | | 708 |
| ATCCTGTGGA | | | 709 |
| CACCTCTCAT | Human lysyl oxidase-like protein mRNA, complete cd | L21186 | 710 |
| GTACCTAGAG | | | 711 |
| CCTGTCTAGC | | | 712 |
| CTCCTGTGCC | Human mRNA for transcriptional activator hSNF2b, c | D26156 | 713 |
| CGGTTTGCAT | | | 714 |
| CCAAGAAGGT | | | 715 |
| CAGAGACGGT | | | 716 |
| CATTTGGCCA | | | 717 |
| CAGGCAGGCT | | | 718 |
| CAGGCCTCTG | | | 719 |
| CAGGGAAGCC | H.sapiens mRNA for human giant larvae homolog. | X87342 | 720 |
| CGCTGTGGGG | | | 721 |
| CGCCTATAGT | | | 722 |
| CGCCGGGGGC | | | 723 |
| CTGCTGATCT | | | 724 |
| CACTGCAGCA | | | 725 |
| CACCTCTCCT | | | 726 |
| AACACGAATG | | | 727 |
| AACTCTCCTA | | | 728 |
| AACTTGATGG | | | 729 |
| AAGATTTTAG | | | 730 |
| AAGCATATGG | | | 731 |
| AAGCTGCAAA | H.sapiens mRNA (clone ICRFp507L1876). | Z69915 | 732 |
| AATACACTTG | | | 733 |
| AAGGACCAGC | | | 734 |
| AAATTGATGC | | | 735 |
| GATGTGACTG | | | 736 |
| AAGTTTGTGG | | | 737 |

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| GATGCTAACC | | | 738 |
| GATGCGTGCC | | | 739 |
| GATCCTTGGT | | | 740 |
| GAGAAAGAGG | H.sapien tyrosinase and mutant tyrosinase, complet | M74314 | 741 |
| AAGGACATTC | Human laminin B2 mRNA, 3' end. | M27654 | 742 |
| AAAAGCTTGA | | | 743 |
| GCCCGGCACG | | | 744 |
| GCCCCTAAAC | | | 745 |
| GCCAGGTTAC | Human mRNA for KIAA0271 gene, complete cds. | D87461 | 746 |
| GCCAAGTTTG | | | 747 |
| GCAGGGCCAG | Human faciogenital dysplasia (FGD1) mRNA, complete | U11690 | 748 |
| GCAGCTCAAA | | | 749 |
| GATTCAACGC | | | 750 |
| GCAGCGCTGG | | | 751 |
| GCACCCACTG | | | 752 |
| AAAGGTGATA | | | 753 |
| AAAGTGGA | Human TFIIID subunit TAFII55 (TAFII55) mRNA, comple | U18062 | 754 |
| GCAGCAGGAA | | | 755 |
| AAATGGCTTG | | | 756 |
| GCACTCCAGC | | | 757 |
| GCACCTCCTA | | | 758 |
| AATGAAAAA | Homo sapiens Rad51C (RAD51C) mRNA, complete cds. | AF0296 | 759 |
| TTTTTGAATA | | | 760 |
| GAGGATTTGG | | | 761 |
| AGGAGAGGGC | | | 762 |
| AGGATTAAAA | | | 763 |
| AGGCCACAA | Homo sapiens alpha-mannosidase (6A8) mRNA, complet | U37248 | 764 |
| AGGCCCTGCT | | | 765 |
| AGGCTCCGTG | Human mRNA for KIAA0223 gene, partial cds. | D86976 | 766 |
| AGGCTGCGCT | | | 767 |
| GAGTGGAGAG | | | 768 |
| AGGGGCGCAG | H.sapiens mRNA for protein containing SH3 domain, | X99656 | 769 |
| AGCAAGTCTC | Human liver 2,4-dienoyl-CoA reductase mRNA, comple | U49352 | 770 |
| GAGGAGTGGG | | | 771 |
| AGTTGTCCCG | Homo sapiens clone 24561 unknown mRNA, partial cds | AF0550 | 772 |
| GAGCCATTTG | | | 773 |

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| ATCCAGGGTC | | | 774 |
| ATCCTGATGG | | | 775 |
| TTTGTGTCAC | Human chromosome 3p21.1 gene sequence, complete cd | L13434 | 776 |
| GAGGCGAGGC | | | 777 |
| ACCTATCCAA | | | 778 |
| AATTTGTGAA | | | 779 |
| ACAGAATGCC | | | 780 |
| ACAGACACTT | | | 781 |
| GAGTCGTAAT | | | 782 |
| GAGTCCGGAG | H.sapiens mRNA for neurotensin receptor. | X70070 | 783 |
| ACCCCAAGG | | | 784 |
| AGCCCTTTTT | Homo sapiens transcription factor (CBFB) mRNA, 3' | L20298 | 785 |
| ACCTACAGCG | | | 786 |
| AGCCAATTGTG | | | 787 |
| ACTGCCCCAA | | | 788 |
| ACTTACCTGG | | | 789 |
| AGAAGGATCT | Homo sapiens mRNA for SPIN protein. | Y14946 | 790 |
| AGAATTTAGG | | | 791 |
| AGACGCACTC | | | 792 |
| AGCAAGCTGC | | | 793 |
| ATGACTAGCG | | | 794 |
| ACCCTGCCAA | | | 795 |
| GCCTCCTCCC | | | 796 |
| GCTCTGGGCG | | | 797 |
| TCTACTTTTG | Human DNA polymerase delta small subunit mRNA, com | U21090 | 798 |
| CTCCACAAAT | | | 799 |
| ATCCAGTCTG | | | 800 |
| CTGCAGGCCC | | | 801 |
| GCCGCCATCT | Human transketolase (TKT) mRNA, complete cds. | U55017 | 802 |
| TGATTAAGGT | | | 803 |
| TTCCTGCCCC | | | 804 |
| AGACCAAAGT | Human mRNA for heat-shock protein 40, complete cds | D49547 | 805 |
| TCCTTCTCCA | Human mRNA for alpha-actinin. | X15804 | 806 |
| CCCCCACCTA | Homo sapiens differentiation-dependent A4 protein | L09604 | 807 |
| AAGGTCGAGC | Human ribosomal protein L30 (homologue of yeast rp | M94314 | 808 |
| AAAAATAAAG | Human novel transcript from adenocarcinoma cell li | U28250 | 809 |
| GGCTCGGGAT | Human mRNA for calcium activated | X04366 | 810 |

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| | neutral protease | | |
| CCAGGAGGAA | | | 811 |
| GCAGTGGCCT | Homo sapiens ezrin-radixin-moesin binding phosphop | AF0159 | 812 |
| TTCCTGACTA | | | 813 |
| CCTTTGCCCT | | | 814 |
| GAAAGAGCTG | Human H2A.X mRNA encoding histone H2A.X. | X14850 | 815 |
| AAGCTGAGTG | Human M4 protein mRNA, complete cds. | L03532 | 816 |
| GTGGCGCACA | 26 S protease subunit 5b=50 kda subunit [human, He | S79862 | 817 |
| CTGGCCCCGA | Homo sapiens encoding vasodilator-stimulated phosp | Z46389 | 818 |
| CTCTCACTCT | | | 819 |
| GAATTTTATA | Human peripheral benzodiazepine receptor (hpbs) mR | M36035 | 820 |
| AGTTTCCCAA | | | 821 |
| TGGCCTCCCC | H.sapiens mRNA for rho GDP-dissociation Inhibitor | X69550 | 822 |
| TGAGAGGGTG | H.sapiens mRNA for HS1 protein. | X57347 | 823 |
| GGGAGCTGCG | | | 824 |
| GACAATGCCA | Human mRNA for ATP synthase gamma-subunit (L-type) | D16562 | 825 |
| CTCCTGGGGC | | | 826 |
| GGTGGCACTC | Homo sapiens RHOA proto-oncogene multi-drug-resist | L09159 | 827 |
| CTGGCCCCGAG | Human GDP-dissociation inhibitor protein (Ly-GDI) | L20688 | 828 |
| ATAGTAGCTT | Human actin bundling protein mRNA, complete cds. | U09873 | 829 |
| AAGAGACAGT | Human RNA polymerase III subunit (RPC62) mRNA, com | U93867 | 830 |
| AAATCGATGA | | | 831 |
| AACACTGACT | | | 832 |
| AACCAATACA | | | 833 |
| AACCACCCAG | | | 834 |
| AACCCAGCC | | | 835 |
| AACCCGGAAG | Human butyrophilin (BTF4) mRNA, complete cds. | U90546 | 836 |
| CCAAACGTGT | Human HepG2 3' region Mbol cDNA, clone hmd1c12m3. | D17130 | 837 |
| AACTTGCCAA | Human high-affinity copper uptake protein (hCTR1) | U83460 | 838 |
| AAACTGAATA | | | 839 |
| AAGATCAAGT | | | 840 |
| AAGGACAGTG | | | 841 |

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| AATAAACGTG | | | 842 |
| AATTCTCCTA | | | 843 |
| AATTTACTTC | Homo sapiens ras GTPase-activating-like protein (I | L33075 | 844 |
| ACAGCCAAGA | Human diadenosine tetraphosphatase mRNA, complete | U30313 | 845 |
| AACTACCAGA | | | 846 |
| GGGGGAATTT | | | 847 |
| GTGAGCCCAT | | | 848 |
| CTAGCTTTTA | | | 849 |
| CCCCCGCGGA | | | 850 |
| CAGATCTTTG | Human UbA52 placental mRNA for ubiquitin-52 amino | X56999 | 851 |
| TAGATAATGG | | | 852 |
| GGCTCCCACT | Human 90-kDa heat-shock protein gene, cDNA, comple | M16660 | 853 |
| AAAGTTTGAG | H.sapiens OB-RGRP gene. | Y12670 | 854 |
| CCCAAGCTAG | Human mRNA fragment for estrogen-regulated 24k pro | X16477 | 855 |
| AAAGAACAGA | | | 856 |
| CATTTGTAAT | Human HepG2 3' region cDNA, clone hmd3c12. | D16914 | 857 |
| GGAGTGGACA | Homo sapiens ribosomal protein L18 (RPL18) mRNA, c | L11566 | 858 |
| ATCACGCCCT | | | 859 |
| TCAGACGCAG | Human prothymosin alpha mRNA, lymphocyte clone pIF | M14794 | 860 |
| TGGCCCCACC | Homo sapiens Opa-interacting protein OIP3 mRNA, pa | AF0254 | 861 |
| AAACAGCTCC | | | 862 |
| GTAAGTGTAC | 12S rRNA [human, rRNA Mitochondrial Partial Mutant | S64650 | 863 |
| ATTAACAAAG | Human guanine nucleotide-binding protein G-s, alph | M14631 | 864 |
| GTGGGAGACC | | | 865 |
| TGGGAAACT | Homo sapiens clone B1-6 zinc finger protein mRNA, | AF0271 | 866 |
| AGGTACTACT | Human epithelium-restricted Ets protein ESX mRNA, | U66894 | 867 |
| AGGGTGAAAC | Human splicing factor SRp30c mRNA, complete cds. | U30825 | 868 |
| ACGCCCTGCT | Homo sapiens protein kinase gene, 3' end of cds an | M94203 | 869 |
| ACCGCAATGC | | | 870 |
| AAGGAAGCAA | Homo sapiens mRNA for nucleolar protein hNop56. | Y12065 | 871 |
| CAGCTGGCCA | H.sapiens mRNA for fibulin-1 C. | X53743 | 872 |

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| TAGTCCCTCT | H.sapiens mRNA for PHAPI2a protein. | Y07569 | 873 |
| CAGGTTGTCC | | | 874 |
| GCAGGGTGGG | | | 875 |
| CAAAAGGCTC | | | 876 |
| ATTCTTCGGA | | | 877 |
| AGGCTGGATG | Homo sapiens clone 23912 mRNA sequence. | AF0381 | 878 |
| ACCGAAACTT | | | 879 |
| ACCCACCCA | Human clone 23552 unknown mRNA, partial cds. | AF0071 | 880 |
| TGACTGGCAG | Human lymphocytic antigen CD59/MEM43 mRNA, complet | M34671 | 881 |
| GAGTGGCTAT | Homo sapiens mRNA for GDP dissociation inhibitor b | Y13286 | 882 |
| TGGTGGACTT | | | 883 |
| TCGGAGAAAA | | | 884 |
| TAAAGGTTTT | Homo sapiens transcriptional coactivator ALY mRNA, | AF0470 | 885 |
| GTTGTAGACT | | | 886 |
| GTCCAGTCTC | | | 887 |
| GGCTCCTTGA | | | 888 |
| CAAGACAGAA | | | 889 |
| GCAGACTCAG | | | 890 |
| TGGGCCTGTG | | | 891 |
| GAGGGCCTTG | H.sapiens TSC2 mRNA for tuberin. | X75621 | 892 |
| CTTCTCAGGG | | | 893 |
| CTCGGTGATG | Homo sapiens mRNA for ras-related GTP-binding prot | D78132 | 894 |
| CTCCTGAAGG | | | 895 |
| CGTGTGCCTG | | | 896 |
| CCCTGGTGGG | | | 897 |
| GCGGAGAGAG | | | 898 |
| GTGGGTGTCC | | | 899 |
| CTGGGAGGAG | Homo sapiens tetraspan (NAG-2) mRNA, complete cds. | AF0228 | 900 |
| CCTGTGGTCC | | | 901 |
| AGAAGTATAG | MB1=proteasome subunit MB1 [human, JY T-cells, mRN | S74378 | 902 |
| AATGAGAAGG | | | 903 |
| GGTAGCCTGG | Homo sapiens Hepatitis B virus X-associated protei | L40326 | 904 |
| ATGTGGCACA | | | 905 |
| TTCGGGTGTG | Homo sapiens protein kinase (HSTPK13) mRNA, comple | L19559 | 906 |
| TTGGCCAGGA | | | 907 |
| GCGCCGCCCC | | | 908 |

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| GACGGCCAGA | | | 909 |
| CGAGGGCACT | Homo sapiens beta III spectrin (SPTBN2) mRNA, part | AF0264 | 910 |
| CCCCCTCGTG | | | 911 |
| AATCTTGTTT | | | 912 |
| AACGCGAACA | Homo sapiens mRNA for IgE autoantigen. | Y14314 | 913 |
| TCACCGGTCA | Human mRNA for plasma gelsolin. | X04412 | 914 |
| ATGTACTCTG | Human inosine-5'-monophosphate dehydrogenase (IMP) | J04208 | 915 |
| GAAACCGAGG | | | 916 |
| ACCCCTGAGA | | | 917 |
| TGATCTGCCT | | | 918 |
| GGGTGGGGTT | | | 919 |
| GGCTGGTCTC | | | 920 |
| GCTGGGGTGG | Human Fas-associating death domain-containing prot | U24231 | 921 |
| GCCAGGAAGC | | | 922 |
| CTTCTACTAA | | | 923 |
| GCACCGCCGG | H.sapiens mRNA for stress activated protein kinase | Y10488 | 924 |
| GCAGGTCAGC | Human branched chain alpha-keto acid dehydrogenase | J04474 | 925 |
| CCTCAGGCTC | Human transcription factor LZIP mRNA, complete cds | U88528 | 926 |
| ATGTAGAGTG | Human mRNA for thymidylate synthase (EC 2.1.1.45). | X02308 | 927 |
| ATCAAGAATC | | | 928 |
| AAGTTGCTAT | Human mutant cerebroside sulfate activator protein | M60258 | 929 |
| AAGAAACTG | | | 930 |
| AAAAGAGAAA | | | 931 |
| TTCGCTGAGG | | | 932 |
| GCAGGAACAG | | | 933 |
| GAGGAATATG | | | 934 |
| ACAGTGCTTG | Human phosphatase 2A mRNA, partial cds. | J03805 | 935 |
| GACATTTGTC | | | 936 |
| GACCACAAAT | | | 937 |
| GACCATTTGA | H.sapiens mRNA for Sec23B isoform, 2450bp. | X97065 | 938 |
| GA CTCTGAAA | | | 939 |
| GAGACTCCAC | | | 940 |
| GACAAGGAAG | Human pancreatic beta cell growth factor (INGAP) m | U41737 | 941 |
| GAGCAGGGTG | | | 942 |

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| GAATAACAT | | | 943 |
| GAGGTCCTTC | | | 944 |
| GATGGTGGAA | | | 945 |
| GATGTTGTCC | | | 946 |
| GATGTTTGAA | | | 947 |
| GATTCTAGCC | | | 948 |
| GATTCTTTTC | Human transposon-like element mRNA. | M23161 | 949 |
| GAGAGGACAG | | | 950 |
| CTGCTTCCTG | | | 951 |
| CTCCAGGACA | H.sapiens mRNA for transketolase-like protein (285 | X91818 | 952 |
| CTCCCTCTGC | | | 953 |
| CTCTGCCCTC | | | 954 |
| CTCTTAATGT | Human homeodomain protein DLX-2 mRNA, 3' end. | L07919 | 955 |
| CTGAAAATTG | | | 956 |
| CTGACCAGAG | | | 957 |
| GACAAATGAGA | H.sapiens mRNA for NAD (H)-specific isocitrate deh | Z68907 | 958 |
| CTGATCCCCC | | | 959 |
| GCATTGATGT | | | 960 |
| CTGTAACATA | Human mRNA for phosphatidylinositol-glycan-class C | D85418 | 961 |
| CTTATTCCTT | Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) | AF0474 | 962 |
| CTTCTGCAAA | | | 963 |
| CTTGGTGTGC | | | 964 |
| GAAAAATTTA | Human unknown protein from clone pHGR74 mRNA, comp | M38188 | 965 |
| GAAGAGTCTC | | | 966 |
| CTGAGCGCCT | | | 967 |
| GGGAAGGGCG | | | 968 |
| GGCAAACCTT | | | 969 |
| GGCAGAGGGC | | | 970 |
| GGCAGCTGGC | | | 971 |
| GGCCCACTAG | Human mRNA for KIAA0095 gene, complete cds. | D42085 | 972 |
| GGCCCCATTT | Human carbonyl reductase mRNA, complete cds. | J04056 | 973 |
| GGCGTTTAGA | | | 974 |
| GATTTTTTCAT | | | 975 |
| GGCTGTGGCC | | | 976 |
| GGAGAGGGCA | | | 977 |
| GGGATCGCCC | | | 978 |
| GGGCAGATGC | | | 979 |
| GGGCAGGACC | | | 980 |

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| GGGCTCCTGT | | | 981 |
| GGGGCAGAGA | Homo sapiens myristoyl CoA:protein N-myristoyltran | AF0205 | 982 |
| GGTTGATCAC | H.sapiens mRNA for -14 gene, containing globin reg | X90857 | 983 |
| GGCTGAGAAT | | | 984 |
| GCCTCTGCCA | Human mRNA for KIAA0272 gene, partial cds. | D87462 | 985 |
| CTCAGGAAGC | Homo sapiens GTPase-activating protein (SIPA1) mRN | AF0297 | 986 |
| GCCAAAACCT | | | 987 |
| GCCAGACGTG | | | 988 |
| GCCCCTGCTG | Human type II keratin K5 mRNA, 3' end. | M19723 | 989 |
| GCCCGCAGGG | Homo sapiens dishevelled 1 (DVL1) mRNA, complete c | AF0060 | 990 |
| GCCGCTCCTG | | | 991 |
| GGAGGGACCT | | | 992 |
| GCCTAGCTGG | | | 993 |
| GGAGCCAGGC | H.sapiens GSTT1 mRNA. | X79389 | 994 |
| GCCTTCAAAC | | | 995 |
| GCCTTGGCAG | Human iroquois-class homeodomain protein IRX-2a mR | U90304 | 996 |
| GCTGCCTACG | | | 997 |
| GCTGGATGCA | | | 998 |
| GCTTAATAGT | | | 999 |
| GGAAAATACT | | | 1000 |
| GCACAGTGAG | Human small GTP-binding protein mRNA, complete cds | U57094 | 1001 |
| GCCGTCGGAG | | | 1002 |
| ATGTTGATTT | | | 1003 |
| ATCACTAAAG | | | 1004 |
| ATCCCTCATC | Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like p | D49396 | 1005 |
| ATCGGCCGTA | | | 1006 |
| ATCTCGGCTC | | | 1007 |
| ATGAAAAGAT | | | 1008 |
| ATGCCTGGTA | | | 1009 |
| CATTTGAAAG | | | 1010 |
| ATGTAGGTGC | Human clone 23748 mRNA, complete cds. | U79294 | 1011 |
| AGTTGGACGG | Human DNA ligase I mRNA, complete cds. | M36067 | 1012 |
| ATTAAAGTGC | | | 1013 |
| ATTGAAAGCA | Human 5-hydroxytryptamine7 receptor isoform d mRNA | U68488 | 1014 |

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| CAAAGCGAGG | | | 1015 |
| CACTCCGCTT | | | 1016 |
| CAGCAGCAAA | | | 1017 |
| CTCATTCAGC | | | 1018 |
| ATGCGGGAGA | | | 1019 |
| AGAAGTACTG | H.sapiens RR1 mRNA for large subunit ribonucleotid | X59617 | 1020 |
| GTACCCGTAC | | | 1021 |
| ACCGGTCCGG | | | 1022 |
| ACGACAAAGC | Homo sapiens clone 23731 peptidylglycine alpha-ami | AF0353 | 1023 |
| ACTATCCTGA | | | 1024 |
| ACTCCAGTCA | | | 1025 |
| ACTGGCGAAT | | | 1026 |
| ATCACACCCC | | | 1027 |
| AGAAGAACGA | Human deoxyhypusine synthase mRNA, complete cds. | U26266 | 1028 |
| ATAAAGTAAC | | | 1029 |
| AGCAGCTTTC | | | 1030 |
| AGCCAGGAGC | | | 1031 |
| AGCCTCTGCC | Homo sapiens katanin p80 subunit mRNA, complete cd | AF0524 | 1032 |
| AGGAAAAGCT | | | 1033 |
| AGGAAAAGTG | | | 1034 |
| AGTCTAGCTA | | | 1035 |
| CCACTCTGGC | H.sapiens mRNA for processing a- glucosidase I. | X87237 | 1036 |
| ACTGGGTGCA | | | 1037 |
| CTACAATTTT | | | 1038 |
| CCTGTGTGCA | | | 1039 |
| CGCCTATAAT | | | 1040 |
| CGCGGGCCCCG | | | 1041 |
| CGGACAGCCA | Homo sapiens clone 24815 unknown mRNA, partial cds | AF0550 | 1042 |
| CGGGATGCAG | | | 1043 |
| CGGGGTTCCTT | | | 1044 |
| CATTGCGGAT | | | 1045 |
| CGTTCTGCGG | | | 1046 |
| CCTGGGCACT | | | 1047 |
| CTACCAGCAC | | | 1048 |
| CTACGAGTGA | glyoxalase I [human, HeLa cells, mRNA Partial, 572 | S83285 | 1049 |
| CTATAGCATA | Human amphiregulin (AR) mRNA, complete cds, clones | M30704 | 1050 |
| CTCAAGCACC | | | 1051 |
| CTCACCTGCT | | | 1052 |

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| ACCATAATGT | | | 1053 |
| CGTCAAGATT | Human farnesyltransferase alpha-subunit mRNA, comp | L10413 | 1054 |
| CCGCTGCTTG | H.sapiens HSJ1 mRNA. | X63368 | 1055 |
| CCCAAAGGCC | Human Treacher Collins syndrome (TCOF1) mRNA, comp | U76366 | 1056 |
| CCCCGATCTT | | | 1057 |
| CCCCTCCCCC | Human velo-cardio-facial syndrome 22q11 region mRN | U84524 | 1058 |
| CCCTCACTCC | | | 1059 |
| CCCTGCTTGT | | | 1060 |
| CCCTGTCTCC | | | 1061 |
| TTAGTTAAGC | H.sapiens mRNA (clone p5) for archain. | X81198 | 1062 |
| CCGCCTTCTC | | | 1063 |
| CCTGGTCCCC | | | 1064 |
| CCGGGCGTGG | | | 1065 |
| CCTAACGTGT | | | 1066 |
| CCTCCTTCCC | Human crystallin beta-B2 mRNA, complete cds. | L10035 | 1067 |
| CCTCTGGCAG | | | 1068 |
| CCTGACCCTG | | | 1069 |
| CCTGCCCACC | Human phenylethanolamine N-methyltransferase mRNA, | J03727 | 1070 |
| CTCAGTCCCC | H.sapiens mRNA for galectin. | Z49107 | 1071 |
| CCGATTTTAA | | | 1072 |
| TGTGACATCC | | | 1073 |
| GTGTCTCCCG | | | 1074 |
| GTGGTGTACA | | | 1075 |
| TGCTGCTGCC | | | 1076 |
| GTGGTGGACG | Human growth/differentiation factor 1 (GDF-1) mRNA | M62302 | 1077 |
| TGGAGCCTAA | | | 1078 |
| TGGCTAAAAA | | | 1079 |
| TGGTAGATGC | | | 1080 |
| GTGGCCGTGG | | | 1081 |
| GTGGCCACCC | | | 1082 |
| TGGTTCTATA | | | 1083 |
| TGTACTTTCC | | | 1084 |
| TGTCAGGAAC | | | 1085 |
| GTGACATCTC | | | 1086 |
| GTGCTGGTAG | | | 1087 |
| GTTATTGTGG | | | 1088 |
| TCTCCTGGAA | | | 1089 |
| TGTGTACTGC | Homo sapiens NBMPR-insensitive nucleoside transpor | AF0341 | 1090 |

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| TATACAGATT | | | 1091 |
| TCTACCTGAT | | | 1092 |
| TTAAAAGTCA | | | 1093 |
| TCGGAGGCCT | | | 1094 |
| TATCTTTATA | | | 1095 |
| TTAGTTCGAC | | | 1096 |
| TTCAAAGGAA | Human mRNA for KIAA0051 gene, complete cds. | D29640 | 1097 |
| TATGAGCACA | | | 1098 |
| TTCCATAGCC | Homo sapiens Notch3 (NOTCH3) mRNA, complete cds. | U97669 | 1099 |
| TTCCCAGCTC | | | 1100 |
| GTGACGTGCA | | | 1101 |
| GTTTGCCTGA | | | 1102 |
| GTTTCCAGGT | Human clone 23627 mRNA, complete cds. | U79266 | 1103 |
| TGACTCTTGA | | | 1104 |
| TAAATTCACC | | | 1105 |
| TAATCCTCAA | | | 1106 |
| TGACCTATTT | | | 1107 |
| TAATTTGCAT | Human epithelial membrane protein (CL-20) mRNA, co | U77085 | 1108 |
| TAAACCTAGG | | | 1109 |
| TAAAAGAGGG | | | 1110 |
| TACACCCGCT | Human DNA repair helicase (ERCC3) mRNA, complete c | M31899 | 1111 |
| GTTTTCAAAA | | | 1112 |
| GTTTGTTTCC | | | 1113 |
| TGAAGAGAAT | Human zinc finger protein RIZ mRNA, complete cds. | U17838 | 1114 |
| TCACAGGGTC | | | 1115 |
| TACATATGGT | | | 1116 |
| TGCGACCGCA | | | 1117 |
| TGAAAGTAAC | Human clone 23711 unknown mRNA, partial cds. | AF0071 | 1118 |
| TAGCAGATTG | Homo sapiens (clone p5-23-3) mRNA. | L48692 | 1119 |
| TACTCAGAGG | | | 1120 |
| GTTGGGTAGA | | | 1121 |
| GTTTAAAAAA | | | 1122 |
| TGCCTGGAAC | | | 1123 |
| GTTTGATTCC | | | 1124 |
| TGCCATTAAG | | | 1125 |
| TGCAAAAAAA | | | 1126 |
| TACGGCTCGC | | | 1127 |
| TGCAGGCTCC | | | 1128 |
| TACCCAGGGC | | | 1129 |

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| TGAAATGAAG | | | 1130 |
| TGCAAATCAG | | | 1131 |
| TGCCTTCAGG | | | 1132 |
| GTTTATGGAT | Human matrix Gla protein (MGP) mRNA, complete cds. | M58549 | 1133 |
| TCATCCCCCA | | | 1134 |
| TTTCCTGTGT | | | 1135 |
| TCAGACTTTG | | | 1136 |
| TCCCTGCCCT | | | 1137 |
| TTTTGAGCTT | | | 1138 |
| TTTCCACACC | | | 1139 |
| TTCTGTGCG | | | 1140 |
| TTTTACATCT | Homo sapiens thyroid receptor interactor (TRIP10) | L40379 | 1141 |
| GGTTTTAGTT | | | 1142 |
| TTTATTTGGC | Human lamin B receptor (LBR) mRNA, complete cds. | L25931 | 1143 |
| TGGAGTGATC | | | 1144 |
| TCACTACTGG | Homo sapiens protein regulating cytokinesis 1 (PRC | AF0445 | 1145 |
| TTTTCTATTT | | | 1146 |
| GTATTCTCTT | | | 1147 |
| TTGTTGGTCA | | | 1148 |
| GGGGTACCCC | | | 1149 |
| TCAACAGCGT | | | 1150 |
| TTCTTGCAGC | | | 1151 |
| TCGGAGCCCC | | | 1152 |
| TTCTTGGGAT | | | 1153 |
| TCCCAGGTCC | Human mRNA for bcr (breakpoint cluster region) gen | X02596 | 1154 |
| TCCGCTTCGG | | | 1155 |
| GGGGGGTGGA | | | 1156 |
| GTCGGACACT | | | 1157 |
| TTGCCTAGGC | | | 1158 |
| TTGGGGAGGG | H.sapiens mRNA for DNA glycosylase. | Y11731 | 1159 |
| TTGCCTTTTT | | | 1160 |
| GGGCCAAAAC | | | 1161 |
| GCTTACCTTT | | | 1162 |
| ATACATTTAG | H.sapiens mRNA for Cl1 protein. | X81625 | 1163 |
| GGAAAGCTGC | | | 1164 |
| GGGACGGCGC | | | 1165 |
| GGTGGAAGCT | | | 1166 |
| GGTGCCCGGC | | | 1167 |
| GGTGCCAAAA | | | 1168 |
| ATGGCAAGGG | | | 1169 |
| GGCCAGGAAG | | | 1170 |

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| GGGGATGGGG | | | 1171 |
| GGCTTTCAGC | | | 1172 |
| GGGCCTTGGA | Human mRNA for platelet-derived growth factor B ch | X02811 | 1173 |
| GGGCCAACCC | | | 1174 |
| GGGGTAAGAA | Human mRNA for human homologue of rat phosphatidyl | D16111 | 1175 |
| GGCTTCCTGG | | | 1176 |
| CCCACCCCA | | | 1177 |
| CTCTGGAAT | | | 1178 |
| CCACTACACT | Human TNF-related apoptosis inducing ligand TRAIL | U37518 | 1179 |
| GTAATCCCCG | | | 1180 |
| CTGCAGACCC | Human peroxisomal enoyl-CoA hydratase-like protein | U16660 | 1181 |
| GGCTCGGGGA | | | 1182 |
| GGTTGTCTAA | | | 1183 |
| GAAAACAAAG | Human acidic keratin-10 mRNA, complete cds. | M19156 | 1184 |
| GAAAAGTTGC | | | 1185 |
| GAAACCCTCA | Human NOF1 mRNA, complete cds. | U39400 | 1186 |
| GAAACTAGGA | Homo sapiens Shab-related delayed-rectifier K+ cha | AF0434 | 1187 |
| GAATCAGAAG | | | 1188 |
| GCGGACCCTG | | | 1189 |
| GAGGGCCGTG | | | 1190 |
| ATTAAGAAAA | | | 1191 |
| GATTATTGGG | Human selenium donor protein (selD) mRNA, complete | U34044 | 1192 |
| GCAGAAAGTT | | | 1193 |
| GCAGAGCCTT | | | 1194 |
| CAGCTATTTC | Human fatty acid binding protein homologue (PA-FAB | M94856 | 1195 |
| GGTTATTTTG | Human mRNA for plasminogen activator inhibitor (PA | X04744 | 1196 |
| GCCACAGAGG | | | 1197 |
| GGGGCAGCCC | | | 1198 |
| GGTGTTGCCG | | | 1199 |
| GGGTTGGCTT | tRNASer(UNC) [human, muscle, MERRF/MELAS overlap s | S79597 | 1200 |
| GGGAAGAGTG | | | 1201 |
| GGGACCGTCA | | | 1202 |
| GCTGCAAAGG | | | 1203 |
| GAGGCCATCC | | | 1204 |
| TCGTAACGAG | | | 1205 |
| GTAGGGTTCC | H.sapiens BDP1 mRNA for protein- | X79568 | 1206 |

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| | tyrosine-phosphata | | |
| AACTCAGCTA | | | 1207 |
| GGGGGCTCCT | Homo sapiens protein tyrosine phosphatase receptor | U71075 | 1208 |
| GGGGGGCAGC | | | 1209 |
| GGGGTGAGCA | | | 1210 |
| TAGTTCCCAG | | | 1211 |
| TTTCTTAATG | | | 1212 |
| GGTCCAATC | | | 1213 |
| TCACTTTCTT | Human TBP-associated factor TAFII80 mRNA, complete | U31659 | 1214 |
| TCATTTTCCT | | | 1215 |
| GGGTAATGTG | | | 1216 |
| TACGGGGGCC | | | 1217 |
| TCCACTGGCC | | | 1218 |
| AAGAGCGCCG | | | 1219 |
| GGTATGGCAG | | | 1220 |
| TTGCGCTGGC | | | 1221 |
| TCTGTGACCT | | | 1222 |
| GGTACGTGGT | | | 1223 |
| TGACTGGTCA | Homo sapiens 59 protein mRNA, 3' end. | L19267 | 1224 |
| TTGAAACTGT | | | 1225 |
| TTCTGGACCC | Human mRNA for proteasome subunit p40 / Mov34 prot | D50063 | 1226 |
| TGCCAGGACA | | | 1227 |
| GGTACACTGC | Human tetracycline transporter-like protein mRNA, | L11669 | 1228 |
| TGTAAGTCTG | Human p62 mRNA, complete cds. | M88108 | 1229 |
| TGTGCTAATA | TSE1=protein kinase A regulatory subunit gene [hum | S54711 | 1230 |
| GGGTAGGGGA | | | 1231 |
| TTGGTGATAC | | | 1232 |
| ACAGTGTGTG | | | 1233 |
| GGTGATAGGG | | | 1234 |
| GGTGACCACC | Human XIST, coding sequence 'd' mRNA (locus DXS399 | X56196 | 1235 |
| GGTGCTGGAG | Homo sapiens mRNA for putative methyltransferase. | AJ2244 | 1236 |
| AGGACACCGC | Human mRNA for C-SRC-kinase. | X59932 | 1237 |
| TAGACAATGC | Homo sapiens clone 23674 mRNA sequence. | AF0381 | 1238 |
| GTCAGGCCTC | | | 1239 |
| GGGGCCCCAA | | | 1240 |
| GTGAGGGCAC | | | 1241 |
| AGAGCATATC | Human transducin beta-1 subunit | M36430 | 1242 |

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| | mRNA, 3' end. | | |
| GTGCGGCTGG | | | 1243 |
| AGAACCTTCA | | | 1244 |
| CTACTGTTGG | Human mRNA for KIAA0312 gene, partial cds. | AB0023 | 1245 |
| GTGTATCTTT | Human splicing factor SC35 mRNA, complete cds. | M90104 | 1246 |
| GGGTTTGAAC | | | 1247 |
| GGTGACAGAG | | | 1248 |
| GGTCGACCTA | | | 1249 |
| GTTTGGAGCT | Human MAP kinase 3b mRNA, complete cds. | U66839 | 1250 |
| TAACTAACAA | Human mRNA for KIAA0107 gene, complete cds. | D14663 | 1251 |
| ACAGCGGCAA | | | 1252 |
| TAAGACTTTG | Homo sapiens casein kinase I gamma 2 mRNA, complet | U89896 | 1253 |
| TACAATAATT | | | 1254 |
| TACATTGCTT | Human (clone E5.1) RNA-binding protein mRNA, compl | L37368 | 1255 |
| TACCCTGGCA | Human beta-actin mRNA, partial cds. | M28424 | 1256 |
| AACTGCCCCA | Homo sapiens amyloid beta-peptide binding protein | U96132 | 1257 |
| AAGATAAACT | Human N33 mRNA, complete cds. | U42349 | 1258 |
| TACGAAGTTC | | | 1259 |
| GTGGAGCGGA | | | 1260 |
| GTGGCCTGCA | | | 1261 |
| ATGCAGAGGT | | | 1262 |
| GTGGCAGTGG | | | 1263 |
| CGCGCGCTGG | | | 1264 |
| GTGGCATACA | | | 1265 |
| GTGGCATTG | | | 1266 |
| GTGGCAAAGA | | | 1267 |
| GTGGCCCCCA | | | 1268 |
| GTGGAGTTTG | | | 1269 |
| GTGGCGGCAC | | | 1270 |
| GTGGCGGCTG | | | 1271 |
| GTGGCGGTCTG | | | 1272 |
| GTGGCTGAGG | | | 1273 |
| GTGGCTTATG | | | 1274 |
| GGCCACTCTA | Human putative tRNA synthetase-like protein mRNA, | U07424 | 1275 |
| CCCTCCTCTC | Human D3-type cyclin (CCND3) mRNA, complete cds. | M90814 | 1276 |
| GTGCCTGCAT | | | 1277 |
| AGCAAGCCCC | | | 1278 |

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|-------------|--|--------|------|
| GGAGGGTGAG | Homo sapiens mRNA, complete cds, clone:RES4-23B. | AB0004 | 1279 |
| GCTGCCCTGA | | | 1280 |
| GCTCTGAAGA | Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH | U39317 | 1281 |
| GTGCAGTTAG | | | 1282 |
| CTCAAAAAAA | | | 1283 |
| GTGCCCCGTGC | | | 1284 |
| ATACAGCCAC | | | 1285 |
| GTGCGCTACT | | | 1286 |
| GTGCTCAGCC | | | 1287 |
| GAGAGGGCAG | | | 1288 |
| GAAGACGAAT | | | 1289 |
| GTGCTGGAGG | | | 1290 |
| CTGGCCGCTC | | | 1291 |
| GTGCCACCA | | | 1292 |
| GTTAQCTGCA | | | 1293 |
| ATGGTTAAAG | | | 1294 |
| TTAAACCTCA | H.sapiens (TL35) mRNA from LNCaP cell line. | X75683 | 1295 |
| GTGTAAAAAA | Human mRNA for transcriptional activator hSNF2a, c | D26155 | 1296 |
| TCTTTCCAGA | H.sapiens hPTPA mRNA. | X73478 | 1297 |
| GTGTCGCATC | | | 1298 |
| GTGGTGGTTA | | | 1299 |
| GTTAATTGCT | | | 1300 |
| GTGGTGGTGT | | | 1301 |
| GTTATATGCC | | | 1302 |
| GTTATGAAGC | Synthetic adenovirus transformed human retina cell | X78338 | 1303 |
| GTTCATAGGT | | | 1304 |
| GTTCGTGCCC | | | 1305 |
| GTTCTGCCGC | | | 1306 |
| GTAAAACCCC | Human fibroblast mRNA fragment with Alu sequence (| X05128 | 1307 |
| GTGTCTGGGA | | | 1308 |
| GTGGTACATA | | | 1309 |
| AGTGGCTGCC | | | 1310 |
| GTGGGAAACG | | | 1311 |
| GTGGGCACCT | Human mRNA for retinol binding protein (RBP). | X00129 | 1312 |
| AGGGAGAGGG | Human isopeptidase T (ISOT) mRNA, complete cds. | U47927 | 1313 |
| AGGGACATAA | | | 1314 |
| GTGGTGTACG | | | 1315 |
| GTGGGCCAGG | Homo sapiens gamma-glutamyl | M24087 | 1316 |

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| | transpeptidase mRNA, 3 | | |
| GGCGCCAAAA | Homo sapiens oriP binding protein (OBP-1) mRNA, 3' | L29095 | 1317 |
| ACCCCTAACA | | | 1318 |
| ACCCACGTCA | Human jun-B mRNA for JUN-B protein. | X51345 | 1319 |
| ACACAGTGTG | | | 1320 |
| GTGGTGACCC | H.sapiens mRNA for 52 kD subunit of transcription | Y07595 | 1321 |
| AAAATTCTGG | | | 1322 |
| GTGGTGGCGT | | | 1323 |
| AGATTATATG | Human mRNA (KIAA00167), partial sequence. | D28589 | 1324 |
| GTCACCCAAA | | | 1325 |
| AATGTCCGAA | | | 1326 |
| AGGTATGGAG | | | 1327 |
| AGGATGACCA | | | 1328 |
| GTATAAACGA | | | 1329 |
| AGCCACCACG | Homo sapiens mRNA for acetyl LDL receptor, complet | D86864 | 1330 |
| ATAGCTGGGG | Homosapiens ERK activator kinase (MEK1) mRNA. | L11284 | 1331 |
| GTCACAGTCC | Human serum response factor (SRF) mRNA, complete c | J03161 | 1332 |
| ATCCCTCCCC | | | 1333 |
| ACTCAATAAA | Human clone JkR1 mRNA downregulated upon T-cell ac | U38441 | 1334 |
| GTCCTGTCTG | Homo sapiens folate carrier mRNA, complete cds. | AF0043 | 1335 |
| GTCGCTGAGA | | | 1336 |
| GTCGGGACAG | | | 1337 |
| ACCACAAATG | | | 1338 |
| GTGCAAATCC | | | 1339 |
| GGCTCCTGTG | | | 1340 |
| CCCGCATAGA | tumor suppressor gene, P16/MTS1/CDKN2=cell cycle n | S78535 | 1341 |
| GTAATGAAGC | | | 1342 |
| CCTGAACTGG | | | 1343 |
| CCTAAACTCA | | | 1344 |
| GTACCAGCCA | | | 1345 |
| GTA CTGTGGG | | | 1346 |
| ATACACTTTG | | | 1347 |
| CCCTGTTGAT | Human stratum comeum chymotryptic enzyme mRNA, co | L33404 | 1348 |
| AATGTAATCA | Human sorcin (SRI) mRNA, complete cds. | L12387 | 1349 |
| CCCAATAAAC | | | 1350 |

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| CCAATGCAGC | | | 1351 |
| CACGCGGGCG | | | 1352 |
| CACCAGCATT | | | 1353 |
| CAACTGTATT | Human nuclear aconitase mRNA, encoding mitochondri | U80040 | 1354 |
| GTAGGTGAGG | | | 1355 |
| CCCTTCTGCC | | | 1356 |
| TACATTCTGT | Human myeloid cell differentiation protein (MCL1) | L08246 | 1357 |
| ACACTCTCCC | | | 1358 |
| TCAGCTGGCC | | | 1359 |
| TCAAGCCATC | | | 1360 |
| TAGTCTTAAC | | | 1361 |
| TAGAATTTTC | | | 1362 |
| GTGACTTTCT | | | 1363 |
| TACATTTTCA | H.sapiens mRNA for Sm protein G. | X85373 | 1364 |
| GTGACCTCCC | | | 1365 |
| GTGAGACCCG | | | 1366 |
| GTGAGTCACG | | | 1367 |
| GTGATAGGAG | | | 1368 |
| GTAGAGCTTG | | | 1369 |
| GGTGTGGGTG | | | 1370 |
| GTGATTCCGC | | | 1371 |
| GTGAGAAGAG | | | 1372 |
| TTGGCCCAGA | Human IL-4-R mRNA for the interleukin 4 receptor. | X52425 | 1373 |
| AATCCAAAGG | Human MAP kinase kinase 6 (MKK6) mRNA, complete cd | U39656 | 1374 |
| GTCTAGTCAA | Human mRNA for KIAA0179 gene, partial cds. | D80001 | 1375 |
| AACACAGCCT | ZA {region between exons 35 and 36 of the compleme | S81585 | 1376 |
| AAAGTGCATC | | | 1377 |
| TTTTGTACTT | | | 1378 |
| TCCTAGCCTG | | | 1379 |
| TTTGCAATTA | Human mRNA for KIAA0193 gene, complete cds. | D83777 | 1380 |
| CTAAGGCGAG | | | 1381 |
| TTGAGAGATG | | | 1382 |
| GTCTCAGTGC | | | 1383 |
| TTCATAGCTG | | | 1384 |
| GTGAACCCGT | | | 1385 |
| GTGAAGTCAG | | | 1386 |
| TGGCAACCTT | | | 1387 |
| TTTGCGTCAC | | | 1388 |
| GGGATTAAAG | Human MUC18 glycoprotein mRNA, | M28882 | 1389 |

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| | complete cds. | | |
| GCTGTGCTGG | | | 1390 |
| GTCAACAGTA | | | 1391 |
| GTACTIONAGT | | | 1392 |
| GCCACTAAAT | Human mRNA for KIAA0377 gene, complete cds. | AB0023 | 1393 |
| GCCCAGACAT | | | 1394 |
| GCCCAGGACC | | | 1395 |
| GCCAAAGGCC | | | 1396 |
| GGGCCAGGG | | | 1397 |
| GCATTCCTCT | | | 1398 |
| GGGAGCCCGG | | | 1399 |
| GGCTGGGCTT | | | 1400 |
| GCCCCTCGAC | | | 1401 |
| GCCCGTCCCT | | | 1402 |
| GCCCGTTGCT | | | 1403 |
| GCGAGTACCA | | | 1404 |
| GCCCAGGGAA | | | 1405 |
| TAAGTAGCAA | | | 1406 |
| TCAGAAGTTC | | | 1407 |
| TCAAATGTCA | | | 1408 |
| GCAGAGCTGA | | | 1409 |
| TATACGCTCA | | | 1410 |
| TAGGGGAGGG | | | 1411 |
| GCAGCCATCG | | | 1412 |
| GTCATCACTG | | | 1413 |
| TAATATTTTT | Human HepG2 partial cDNA, clone hmd6b09m5. | D17110 | 1414 |
| GCTGCGGTCC | Human HepG2 partial cDNA, clone hmd2h09m5. | D17015 | 1415 |
| GCAGCGCCTG | | | 1416 |
| GTGGTGCGTG | Homo sapiens X-ray repair cross- complementing prot | AF0355 | 1417 |
| GTGGCACCTG | | | 1418 |
| GCAGGAAATA | | | 1419 |
| GTGAACACAG | | | 1420 |
| GTCTACAATT | | | 1421 |
| TACAACAGCA | Human non-lens beta gamma-crystallin like protein | U83115 | 1422 |
| GCGAGACCCC | | | 1423 |
| GCTTTGGGGT | | | 1424 |
| GAGCGGCTCT | | | 1425 |
| GCCTTCGGCG | | | 1426 |
| GACTTCTGAG | | | 1427 |
| GCCTTGATCT | | | 1428 |
| GCCTTGGGGG | | | 1429 |

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| GAGTCTGTTC | | | 1430 |
| GCGAAACTCC | | | 1431 |
| GATCCCCAAC | | | 1432 |
| GCGAGCAGCG | | | 1433 |
| CTTCCGTAGC | | | 1434 |
| CTTAAGACTT | | | 1435 |
| CTGTGGTAGC | | | 1436 |
| GCGAGGCCCC | | | 1437 |
| GGCCTGCAGT | | | 1438 |
| GAATGCTGAC | Homo sapiens lysosomal pepstatin insensitive prote | AF0174 | 1439 |
| GCCTACACGT | | | 1440 |
| GCCCTAATTG | | | 1441 |
| GCCCTCAGGG | | | 1442 |
| GCCCTGTAGT | | | 1443 |
| GCGCGGGCGA | | | 1444 |
| GCGAATTCCC | | | 1445 |
| GCCGACAAGG | | | 1446 |
| GCCTTCAAAA | H.sapiens mRNA for serine/threonine protein kinase | X97630 | 1447 |
| GCCGGCTCTT | | | 1448 |
| GCACTTTGAG | | | 1449 |
| GCCCTGTAAT | | | 1450 |
| GCCTCTCTAC | Human mRNA for glutathione-insulin transhydrogenas | X07077 | 1451 |
| GCCTGAGTGC | | | 1452 |
| GCCTGCCTGG | | | 1453 |
| GCCTGCTCAG | | | 1454 |
| GATGCGCTTG | | | 1455 |
| GCCGTGAGCA | | | 1456 |
| GAGGGGAGTT | | | 1457 |
| GCAGAGACAA | | | 1458 |
| AAGGAACTTG | | | 1459 |
| GAGCTCTGAG | | | 1460 |
| GAGCTTACCC | | | 1461 |
| AAGAGCCAAG | | | 1462 |
| AACTTTCTGG | | | 1463 |
| AAGTAGAGCA | Human ZP3 protein (ZP3) mRNA, complete cds. | M60504 | 1464 |
| AACCGGGAAG | | | 1465 |
| GAGCAGCCCT | | | 1466 |
| AACCAGAATG | | | 1467 |
| GAGGGTGCGA | | | 1468 |
| AAAGAGTCGG | | | 1469 |
| AAAGAAACCC | | | 1470 |
| GAGTCGGCCC | | | 1471 |

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| GAGTGAAATT | | | 1472 |
| GAGGCCGGAG | | | 1473 |
| GAGAGGGGGT | | | 1474 |
| ACCTTAATGG | | | 1475 |
| GAGAAAAAAA | | | 1476 |
| ACCTGAAGCG | Human mRNA for KIAA0323 gene, partial cds. | AB0023 | 1477 |
| GAGAAGATCT | | | 1478 |
| GAGAAGTTGA | | | 1479 |
| GAGAATGGGA | | | 1480 |
| GAGCCTAGGA | | | 1481 |
| ACCCAGGTT | | | 1482 |
| TTTGTTCAAT | Homo sapiens HnRNP F protein mRNA, complete cds. | L28010 | 1483 |
| ACCACAAATA | | | 1484 |
| GAGCACATTT | | | 1485 |
| AATTAAGTCC | | | 1486 |
| GAGCACTGTT | | | 1487 |
| AAGTTGGTGC | | | 1488 |
| AAGTCATAGG | Human autocrine motility factor receptor mRNA. | M63175 | 1489 |
| GAGAGCACCC | | | 1490 |
| TGAATGGCCT | | | 1491 |
| GATTGTAAGG | | | 1492 |
| GCAACTTGTC | | | 1493 |
| TGCTCTGTGT | H.sapiens mRNA for supt5h protein. | Y12790 | 1494 |
| TGCCTTACTT | | | 1495 |
| GCAAGAAGAA | | | 1496 |
| TGCAATAAGC | | | 1497 |
| AAAAATAAAA | Human SnRNP core protein Sm D3 mRNA, complete cds. | U15009 | 1498 |
| TGACCTTACC | | | 1499 |
| TGTATGGTGG | | | 1500 |
| GCACAGTGGG | | | 1501 |
| GCACCCACCC | | | 1502 |
| GCACCTCCAC | | | 1503 |
| TCTGAATCGG | | | 1504 |
| TCTCTGCTCA | | | 1505 |
| CTGGCAGATT | | | 1506 |
| TGAGTGGACA | | | 1507 |
| GATACTAGTG | | | 1508 |
| GCAGAAGCGT | | | 1509 |
| TTTGCGTCCG | | | 1510 |
| TTTGCGGTCC | | | 1511 |
| GAGTTCGACT | | | 1512 |
| TTTACAGCCC | Homo sapiens nuclear dual-specificity | U93181 | 1513 |

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| | phosphatase | | |
| GATAAATTAA | | | 1514 |
| GATTGGCCTT | | | 1515 |
| TTCAGTGCCC | | | 1516 |
| TGTATAGCTT | | | 1517 |
| GATACTGAGG | | | 1518 |
| GATAGAACCA | | | 1519 |
| TGTTGTGCGC | | | 1520 |
| GATCCAGGCT | | | 1521 |
| GATCTCCGTG | | | 1522 |
| GATGCTTTCT | | | 1523 |
| GAGTGTTTCT | Human rho mRNA (clone 12). | X05026 | 1524 |
| TTCTCTACAC | Human TSC-22 protein mRNA, complete cds. | U35048 | 1525 |
| GTGATGGGCT | | | 1526 |
| GCTGCCCCGGC | | | 1527 |
| TAGAAGATGC | | | 1528 |
| TAAACGTGGC | | | 1529 |
| TAAACATTGT | | | 1530 |
| GGATGAGTAC | | | 1531 |
| GTGTGTAAAA | | | 1532 |
| TATTGACAAC | Human X104 mRNA, complete cds. | L27476 | 1533 |
| GGATTTTGGT | Human potassium channel mRNA, complete cds. | U33839 | 1534 |
| GGATGAAACA | | | 1535 |
| GTCTTCTCTG | Homo sapiens membrane-associated kinase (Myt1) mRN | AF0141 | 1536 |
| GGGGTGGGGC | Human CAD mRNA for multifunctional protein CAD, co | D78586 | 1537 |
| GGCAACAAAA | | | 1538 |
| GGGGACGGCC | | | 1539 |
| GGATCAAGTC | Human damage-specific DNA binding protein p48 subu | U18300 | 1540 |
| CTGTCAGCGG | | | 1541 |
| GGATGCAAGG | Human B lymphocyte serine/threonine protein kinase | U07349 | 1542 |
| TGCCCAGGAT | | | 1543 |
| TGGTGTTGAA | | | 1544 |
| TGGGGCAAAG | | | 1545 |
| GGACCACCCA | | | 1546 |
| TGGCCCCCAC | | | 1547 |
| TGGCACTTCA | Human low-Mr GTP-binding protein Rab32 (RAB32) mRN | U71127 | 1548 |
| TGGATTTCAC | | | 1549 |
| TATATTTTCT | Human transglutaminase mRNA, 3' untranslated regio | M98479 | 1550 |

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| TGCCTCTGTC | Human purine nucleoside phosphorylase (PNP) mRNA, | K02574 | 1551 |
| GCTCCACTGG | Human cation-dependent mannose 6-phosphate-specifi | M16985 | 1552 |
| GGAGCTGTGA | | | 1553 |
| TGAGGTGAAG | | | 1554 |
| GGAGGCATCA | H.sapiens (xs11) mRNA, 393bp. | Z36777 | 1555 |
| GGAGTGGAAC | | | 1556 |
| GGATAAATGC | H.sapiens mRNA for nuclear pore complex protein hn | Z25535 | 1557 |
| TCCTCTACCT | | | 1558 |
| GGACTTCTGT | | | 1559 |
| CCTGCCCCCC | Human extracellular signal-regulated kinase 1 mRNA | M84490 | 1560 |
| GGCAACAAGA | | | 1561 |
| GGCCTGGCCT | | | 1562 |
| CTAACTCAGT | | | 1563 |
| CTAAAGACTT | | | 1564 |
| GGCTCAAAAC | | | 1565 |
| GGCTCCACAG | | | 1566 |
| GTTCTGTGTA | | | 1567 |
| CCTGGCTAAT | | | 1568 |
| CTTACGTGAT | | | 1569 |
| CCTGCAATCC | | | 1570 |
| CCTGAGGTCA | | | 1571 |
| CCTGAAATTT | Human heterogeneous ribonucleoprotein A0 mRNA, com | U23803 | 1572 |
| CCGAGGCTTG | Human melanoma-associated antigen p97 (melanotrans | K03200 | 1573 |
| GGCTCCCCAC | | | 1574 |
| CCCTACAACG | | | 1575 |
| CCTGTCCAGT | | | 1576 |
| GACCTCCTGC | Human protein kinase (MLK-3) mRNA, complete cds. | L32976 | 1577 |
| GCCTGTGCTG | Homo sapiens Huntington's Disease (HD) mRNA, compl | L12392 | 1578 |
| GGCAATGGAG | | | 1579 |
| GGCAGTGCCC | | | 1580 |
| GGCATTITTC | | | 1581 |
| GGCCACAGAG | | | 1582 |
| GAGGTCACCA | | | 1583 |
| CTCTTCACGG | Human mRNA for alanyl-tRNA synthetase, complete cd | D32050 | 1584 |
| GGCCACGTAG | | | 1585 |
| GGAACITTTA | | | 1586 |
| GACCACGAAT | Human mRNA for cathepsin H (EC | X16832 | 1587 |

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| | 3.4.22.16). | | |
| GGCCCCCAAT | | | 1588 |
| GGCCCCTCCC | | | 1589 |
| GAAAAGGGTT | | | 1590 |
| CTTTCTTCCC | H.sapiens ERF-1 mRNA 3' end. | X79067 | 1591 |
| CTTCTGTTTT | | | 1592 |
| GAGGCCAACA | Homo sapiens Pig3 (PIG3) mRNA, complete cds. | AF0103 | 1593 |
| GCTAGACCCT | | | 1594 |
| TGTGACCTCT | | | 1595 |
| CCCAATACTC | | | 1596 |
| CCAAGGGCCC | Human mRNA for LZTR-1, complete cds. | D38496 | 1597 |
| CATTTAGATT | | | 1598 |
| CAGTGATTCC | | | 1599 |
| CAGGTGCTGT | Human putative cyclin G1 interacting protein mRNA, | U61836 | 1600 |
| GCGGGGCGAG | | | 1601 |
| CAGCTTCACC | Human nuclear RNA helicase, complete cds. | U90426 | 1602 |
| GCGGGCAACT | | | 1603 |
| CACCTGTAGT | Human ribosomal protein L5 pseudogene mRNA, comple | U66589 | 1604 |
| CACCCCTGAT | Human creatine kinase-B mRNA, complete cds. | M16364 | 1605 |
| CAATTAAAGT | | | 1606 |
| GCTAGCCTCA | | | 1607 |
| GCTAGGAAAC | | | 1608 |
| GCTAGGTATT | | | 1609 |
| GCGTTTAATG | | | 1610 |
| CCTTGGTGCC | H.sapiens MLN62 mRNA. | X80200 | 1611 |
| CTGCCCGCCT | | | 1612 |
| GCGCACCGCT | | | 1613 |
| CTCTCAATAT | | | 1614 |
| GCGCCTCAAC | | | 1615 |
| CTCATAAAAA | | | 1616 |
| CGTGAAAAAA | | | 1617 |
| CCCACGGTTA | H.sapiens mRNA for yeast methionyl-tRNA synthetase | X94754 | 1618 |
| GCGCGATGCA | | | 1619 |
| ATGGCCATAG | H.sapiens mRNA for Ste20-like kinase. | X99325 | 1620 |
| GCGGACACTC | Homo sapiens (clone S53) mRNA, 3' end of cds. | L40398 | 1621 |
| CCTCGTCTTC | | | 1622 |
| GCGGCCCTAG | | | 1623 |
| CCCTTCGTCC | | | 1624 |

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| GCGGCCGTGG | | | 1625 |
| GCGGCGCCGC | | | 1626 |
| CGTCTTCTCT | transcript ch4822 [human, RF1,RF48 stomach cancer | S77362 | 1627 |
| GCTTCCGAGG | | | 1628 |
| GCTGTTGGTG | Homo sapiens partial mRNA for jagged2 protein. | Y14330 | 1629 |
| GCTTATAAAA | | | 1630 |
| GCTTCACTCG | | | 1631 |
| GCTTCCACGA | | | 1632 |
| GCTTCCAGCT | | | 1633 |
| AACACATCAG | Human ataxin-2 (SCA2) mRNA, complete cds. | U70323 | 1634 |
| GCTCACTGCG | | | 1635 |
| AAAGCATTTT | | | 1636 |
| GCTGACGGAA | Human mRNA for phosphoethanolamine cytidyltransf | D84307 | 1637 |
| GCTTGGTACT | | | 1638 |
| GGAAAAATTA | | | 1639 |
| TTTCTACTCA | | | 1640 |
| TTGGGGAAAC | Human biliverdin-IXalpha reductase mRNA, complete | U34877 | 1641 |
| GGAAATTGTT | | | 1642 |
| GGCTCCCTGA | | | 1643 |
| AAAGGTGGAG | | | 1644 |
| AGGAAAGCCA | Homo sapiens mRNA for Rab9 effector p40, complete | Z97074 | 1645 |
| TGTGGCACTG | | | 1646 |
| GCTCCATCTA | | | 1647 |
| ATCTTAGTCA | Homo sapiens mRNA for KIAA0521 protein, partial cd | AB0110 | 1648 |
| GCTCCCGCCC | | | 1649 |
| ATCCCCCTGG | | | 1650 |
| AGTTTTACAA | Human HepG2 partial cDNA, clone hmd5c06m5. | D17081 | 1651 |
| GCTGAGTGCA | | | 1652 |
| AGTAGTCTGC | | | 1653 |
| ACTGGTATAC | Human guanosine 5'-monophosphate synthase mRNA, co | U10860 | 1654 |
| AGCTCACTCC | Homo sapiens Pig10 (PIG10) mRNA, complete cds. | AF0103 | 1655 |
| AGCCTTCCTA | | | 1656 |
| AGATGAGATG | Human DNA-binding protein CPBP (CPBP) mRNA, partia | U44975 | 1657 |
| GCTCTGGTGT | Human mRNA for KIAA0309 gene, partial cds. | AB0023 | 1658 |

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| GCTGACCCTG | | | 1659 |
| ACTTCTGCCC | Human mRNA for muscle phosphofructokinase (E.C. 2. | Y00698 | 1660 |
| ATTCCAAGGA | | | 1661 |
| GCTCGGCCGC | | | 1662 |
| ACTGAGGAAA | insulin-like growth factor binding protein 3 {3' r | S56205 | 1663 |
| TGGCCTAGGG | | | 1664 |
| TGTCTGTGGT | | | 1665 |
| TTCTCCCGCT | Human protective protein mRNA, complete cds. | M22960 | 1666 |
| TTGTTCGATGG | | | 1667 |
| TTAGCCCATC | | | 1668 |
| ATCCACATCG | | | 1669 |
| CAGCATCTAA | | | 1670 |
| TTAGCCAGGC | Human mRNA for tyrosine aminotransferase (TAT) (EC | X52520 | 1671 |
| GGAGGTGGGG | Homo sapiens clone 24720 epithelin 1 and 2 mRNA, c | AF0550 | 1672 |
| TTAGCATTTG | | | 1673 |
| GTGACAACAC | Human voltage-dependent anion channel isoform 1 (V | L06132 | 1674 |
| TGGGTGGGGG | | | 1675 |
| TTAGATCGTT | Homo sapiens tetraspanin Tspan-6 (TSPAN-6) mRNA, c | AF0534 | 1676 |
| CTTGTGAACT | | | 1677 |
| TGGCCTGCCC | | | 1678 |
| GTGAAACCTC | | | 1679 |
| TTAAACATA | | | 1680 |
| CGGCTGAATT | | | 1681 |
| TTAAACATAA | | | 1682 |
| ATTATCCAGG | | | 1683 |
| ACGATTGATG | | | 1684 |
| AAGAAGACTT | | | 1685 |
| ACTCTGCCAA | | | 1686 |
| TGGCCATCTG | | | 1687 |
| CGCCTGTAAT | H.sapiens P1-Cdc21 mRNA. | X74794 | 1688 |
| CCGTGGTCGT | Human fibrillarin (Hfib1) mRNA, complete cds. | M59849 | 1689 |
| CAGGCTTCCA | | | 1690 |
| TTAACATAAG | | | 1691 |
| GCAACGGGCC | Human acyl-CoA thioester hydrolase mRNA, complete | U91316 | 1692 |
| AAGGCCTTGT | | | 1693 |
| CGGCTGGTGA | Human mRNA for proteasome subunit HC5. | D00761 | 1694 |

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| TTCACAGCAG | | | 1695 |
| TTCGGACACT | | | 1696 |
| TTCTGAAGAC | | | 1697 |
| TTGAAAATGT | | | 1698 |
| GATGGGGACA | Human Dr1-associated corepressor (DRAP1) mRNA, com | U41843 | 1699 |
| ACGTGGTGAT | | | 1700 |
| TTGAAGTCAA | Homo sapiens (clone cc33) S182 mRNA, complete cds. | L42110 | 1701 |
| TTCGCTGTCTG | | | 1702 |
| CCTTCCAAAT | Homo sapiens malate dehydrogenase precursor (MDH) | AF0474 | 1703 |
| TCTGGTTTGT | | | 1704 |
| TCTGGTCTGG | Human surface antigen mRNA, complete cds. | M60922 | 1705 |
| GCAAAACCCC | Homo sapiens tumor necrosis factor superfamily mem | AF0365 | 1706 |
| TGAGGCCTCT | | | 1707 |
| TACCTACTGA | | | 1708 |
| GA CTGCGCGT | | | 1709 |
| TTCAGGAGGG | Homo sapiens mRNA for T-cell receptor alpha, clone | Y16433 | 1710 |
| TGTTTGTGTG | | | 1711 |
| GAGCCGCCTC | | | 1712 |
| GAGAGTGTCT | TIMP-1=metalloproteinase inhibitor [human, keratoc | S68252 | 1713 |
| CAGGAGTTCA | Human BRCA2 region, mRNA sequence CG037. | U50523 | 1714 |
| AGGGAAAGAG | edg-2=maternal transcript G10 homolog [human, umbi | S77329 | 1715 |
| TTAGCTGAGT | Human cytochrome B561, HCYTO B561, mRNA, partial c | U06715 | 1716 |
| TTCACTGCTA | Human lipoma cell line Li-14/SV40 ectopic sequence | U29116 | 1717 |
| GGGCAGCTGG | | | 1718 |
| CAGGAGGAGT | Human mRNA for phospholipase C-alpha, complete cds | D16234 | 1719 |
| CAGCTCATCT | | | 1720 |
| AAGTGATTCT | Human mRNA for ZFM1 protein, complete cds. | D26120 | 1721 |
| TTCCATATAC | | | 1722 |
| TGCCCCCGGG | | | 1723 |
| TTCCCTGTCA | | | 1724 |
| GTGGACCCCA | Human siah binding protein 1 (SiahBP1) mRNA, parti | U51586 | 1725 |
| TGGCGCCGAT | | | 1726 |
| TGGGCTGTGT | | | 1727 |

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| TGGGCCAAAC | | | 1728 |
| TGATCTCCAA | fatty acid synthase {3' region} [human, breast and | S80437 | 1729 |
| TGGGAGGGAG | | | 1730 |
| AGACAGAGTG | | | 1731 |
| ATCAAGTGGA | Human mRNA for KIAA0233 gene, complete cds. | D87071 | 1732 |
| TGGGAGCCCT | | | 1733 |
| CTCGAGGAGG | Human ribosomal protein L23-related mRNA, complete | U26596 | 1734 |
| CTGACACAGA | | | 1735 |
| TGGGACAGTT | | | 1736 |
| GCCTAGATAG | | | 1737 |
| TGGCTGTGAG | Human chromosome 17q12-21 mRNA, clone pOV-3, parti | U18920 | 1738 |
| GGGAAGTCAC | Human FX protein mRNA, complete cds. | U58766 | 1739 |
| CTTGATTCCC | Homo sapiens quiescin (Q6) mRNA, complete cds. | U97276 | 1740 |
| TGGAGCGTCC | | | 1741 |
| TGGAAACTGA | | | 1742 |
| TGGAAATCAA | | | 1743 |
| TGGAAGAGCT | | | 1744 |
| TGGACCTGGA | | | 1745 |
| CCCCCAGATG | | | 1746 |
| TGGCGCTGGC | | | 1747 |
| AGCCTGCTCA | Human placental cDNA coding for 5'nucleotidase (EC | X55740 | 1748 |
| GTGCTATTCT | | | 1749 |
| AAGGTAGCAG | | | 1750 |
| TGGAGGCCCA | | | 1751 |
| TTGAGCCAGC | Human FUSE binding protein 2 (FBP2) mRNA, partial | U69126 | 1752 |
| TGAGGGGTGA | Human Gps1 (GPS1) mRNA, complete cds. | U20285 | 1753 |
| TCCACGCACC | | | 1754 |
| TGGGTGCACA | | | 1755 |
| CCCAGGGAGA | Homo sapiens chaperonin containing t-complex polyp | AF0262 | 1756 |
| TGTTACCTGT | | | 1757 |
| TAGGGCAATC | | | 1758 |
| TGTGGGTATT | | | 1759 |
| TGTGGGTCAC | | | 1760 |
| ACCCCCCGC | Human junD mRNA. | X56681 | 1761 |
| AAGTTTCCAA | H. sapiens mRNA for protein phosphatase X. | X70218 | 1762 |

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| TGTGCACACA | | | 1763 |
| TGTGGTGGCA | | | 1764 |
| TGTGAGGGAA | | | 1765 |
| TCTGTTTACT | Human methylenetetrahydrofolate dehydrogenase- | J04031 | 1766 |
| TGTTAGCCTG | | | 1767 |
| GCGACAGCTC | | | 1768 |
| GCCAACCTCC | | | 1769 |
| TGTTTGCCAG | | | 1770 |
| GACTAAGAAA | Human hepatitis delta antigen interacting protein | U63825 | 1771 |
| AAACTGAGA | Homo sapiens CTG repeat mRNA. | L48984 | 1772 |
| TGTCAATGGG | | | 1773 |
| GGGTTTTTAT | Human nuclease sensitive element binding protein-1 | M85234 | 1774 |
| TGGTGAACAG | | | 1775 |
| CTAATAAATG | | | 1776 |
| TGGTTTTGTA | Human mRNA for KIAA0175 gene, complete cds. | D79997 | 1777 |
| ATGGCCAACT | | | 1778 |
| ATCAAGTTCG | | | 1779 |
| TGTAGAATTT | Homo sapiens unknown protein IT12 mRNA, partial cd | AF0409 | 1780 |
| GTGGCGTGTG | Human clone 23933 mRNA sequence. | U79273 | 1781 |
| TGTCCACCCT | | | 1782 |
| TGTCCCAGAG | | | 1783 |
| GGCCATCTCT | | | 1784 |
| GCGAAACCCT | c-erbB3=receptor tyrosine kinase (alternatively sp | S61953 | 1785 |
| TGTCCTGACC | | | 1786 |
| TGTCCTTGAG | Homo sapiens KIAA0441 mRNA, complete cds. | AB0079 | 1787 |
| TGTAAAAAAA | | | 1788 |
| TTTCCTTACA | | | 1789 |
| TACAAGAGGA | neoplasm-related C140 product [human, thyroid carc | S71022 | 1790 |
| CTAGCCTCAC | Human mRNA for cytoskeletal gamma-actin. | X04098 | 1791 |
| CGCCGACGAT | Human interferon-inducible mRNA fragment (cDNA 6-1 | X02492 | 1792 |
| ACTTTCCAAA | | | 1793 |
| GTA CTGTGGC | Human nuclear chloride ion channel protein (NCC27) | U93205 | 1794 |
| GTGCACTGAG | Human mRNA for HLA class-I (HLA-A26) heavy chain, | D32131 | 1795 |
| GCAAGCCAAC | | | 1796 |

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| TTTGGACAAT | | | 1797 |
| TCTGTACACC | Human mRNA for ribosomal protein S11. | X06617 | 1798 |
| TTTGCAAAAA | | | 1799 |
| GTGACAGAAG | Human mRNA for eukaryotic initiation factor 4A1. | D13748 | 1800 |
| TTTGATAATG | | | 1801 |
| CCTCGGAAAA | H.sapiens gene for ribosomal protein L38. | Z26876 | 1802 |
| TTGTTGTTGA | Human mRNA for calmodulin, complete cds. | D45887 | 1803 |
| TTTATTTTGA | | | 1804 |
| TTGACTCCTG | | | 1805 |
| TTTACAGAGG | | | 1806 |
| TTTATAACTT | | | 1807 |
| TGTGCTCGGG | Human mRNA for KIAA0088 gene, partial cds. | D42041 | 1808 |
| GCCACACCCC | | | 1809 |
| GACGTGTGGG | Human histone (H2A.Z) mRNA, complete cds. | M37583 | 1810 |
| AAGCCAGCCC | Human 80K-H protein (kinase C substrate) mRNA, com | J03075 | 1811 |
| GCCTGCAGTC | Homo sapiens Kunitz-type protease inhibitor (kop) | AF0272 | 1812 |
| GCTGAACGCG | | | 1813 |
| TTTCACAGGC | | | 1814 |
| TTTCACCAAGT | | | 1815 |
| CACGCAATGC | Human homolog of Drosophila enhancer of split m9/m | U04241 | 1816 |
| TTTCAGTGGG | | | 1817 |
| GGACTCTGGA | Human mRNA for zinc-alpha2-glycoprotein, complete | D90427 | 1818 |
| CCTCAGCCCG | Human squamous cell carcinoma of esophagus mRNA fo | D43772 | 1819 |
| CACTCAATAA | Homo sapiens serine protease mRNA, complete cds. | AF0139 | 1820 |
| TTTGTAATAT | Human grancalcin mRNA, complete cds. | M81637 | 1821 |
| GCCGGGTGGG | Human collagenase stimulatory factor (EMMPRIN) mRN | L10240 | 1822 |
| ACCCTTGGCC | Homo sapiens mRNA from HIV associated non-Hodgkin' | Y16704 | 1823 |
| CCGTCCAAGG | Human ribosomal protein S16 mRNA, complete cds. | M60854 | 1824 |
| TTTTGTAGAG | Human mRNA fragment for phosphoprotein p53. | X01405 | 1825 |
| TTTTCTCTGA | | | 1826 |

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| TTTTGTTTT | | | 1827 |
| GACATCAAGT | Human mRNA for keratin 19. | Y00503 | 1828 |
| GCTTTATTTG | Human mRNA fragment encoding cytoplasmic actin. (i | V00478 | 1829 |
| GCGACCGTCA | Human fructose 1,6-diphosphate aldolaseA mRNA, 5' | M21190 | 1830 |
| ACTAACACCC | Human PACAP type-3/VIP type-2 receptor mRNA, compl | U18810 | 1831 |
| ATTTGAGAAG | | | 1832 |
| TTTTTACAGT | | | 1833 |
| GATCCCAACT | Human metallothionein II mRNA, partial cds. | M26637 | 1834 |
| TTTTGTTAAT | | | 1835 |
| CCTGGAAGAG | Human thyroid hormone binding protein (p55) mRNA, | J02783 | 1836 |
| GAGTTCGACC | | | 1837 |
| GCCTACCCGA | Human mRNA for pancreatic carcinoma marker GA733-1 | X13425 | 1838 |
| AGCAGGAGCA | Homo sapiens clone DT1P1A7 mRNA, CAG repeat region | U92985 | 1839 |
| GAGAGCTCCC | | | 1840 |
| CTGTACAGAC | | | 1841 |
| TTTTCTCTGC | Human tyk2 mRNA for non-receptor protein tyrosine | X54637 | 1842 |
| TTATGGGATC | Human MHC protein homologous to chicken B complex | M24194 | 1843 |
| GCGGCGCTGC | | | 1844 |
| TTTGTCTGG | | | 1845 |
| TTTGTTCGCA | | | 1846 |
| GTGCGCTGAG | Human mRNA for HLA class I locus C heavy chain. | X58536 | 1847 |
| AACGACCTCG | Human mRNA fragment encoding beta-tubulin. (from c | V00599 | 1848 |
| TTTACTCAC | Human mRNA for erythrocyte adducin alpha subunit. | X58141 | 1849 |
| TTCTTGTGGC | | | 1850 |
| AGGAAGGAAC | Human tyrosine kinase-type receptor (HER2) mRNA, c | M11730 | 1851 |
| TTGCATTAAA | | | 1852 |
| GAAGCCAGCC | Human 4E-binding protein 1 mRNA, complete cds. | L36055 | 1853 |
| TTGCTGTGTG | | | 1854 |
| TGCTTGTCCC | Homo sapiens clone 24614 ADP-ribosylation factor 1 | AF0550 | 1855 |
| CCCACACTAC | Human transducin beta-2 subunit mRNA, complete cds | M36429 | 1856 |
| TAGCTGAGAC | Human nuclear localization sequence | U28386 | 1857 |

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| | receptor hSRP1 | | |
| CCACCCCGAA | H.sapiens TEGT gene. | X75861 | 1858 |
| CGGCCCAACG | H.sapiens mRNA for arginine methyltransferase, spl | Y10805 | 1859 |
| TTGCTCACAC | | | 1860 |
| TTGCCTTGTA | | | 1861 |
| ATCCGCGAGG | | | 1862 |
| TCAGATGGCG | Homo sapiens hD54+ins2 isoform (hD54) mRNA, comple | AF0044 | 1863 |
| AAAGCACAAG | Human 56k cytoskeletal type II keratin mRNA. | J00269 | 1864 |
| CCGGGCCCCAG | Homo sapiens mRNA for TRIP6 (thyroid receptor inte | AJ0019 | 1865 |
| GGCCCTGAGC | Human RNA polymerase II subunit (hsRPB10) mRNA, co | U37690 | 1866 |
| TGCGCTGGCC | | | 1867 |
| GGCCAAAGGC | Human mRNA for KIAA0064 gene, complete cds. | D31764 | 1868 |
| GAAACAAGAT | Human phosphoglycerate kinase (pgk) mRNA, exons 2 | L00160 | 1869 |
| TTGAGTGCAG | | | 1870 |
| GCCGCCCTGC | Human mRNA for very-long-chain acyl-CoA dehydrogen | D43682 | 1871 |
| TTGATGATAA | | | 1872 |
| CTTGTAATCC | | | 1873 |
| AAAGCCAAGA | H.sapiens mRNA for electron transfer flavoprotein | X71129 | 1874 |
| TTGCCTTGCT | | | 1875 |
| TCTTCTCCCT | Human mRNA for hepatoma-derived growth factor, com | D16431 | 1876 |
| GTACGTCCCA | Human neutral amino acid transporter B mRNA, compl | U53347 | 1877 |
| CGGATAACCA | Human cell cycle protein p38-2G4 homolog (hG4-1) m | U59435 | 1878 |
| GTCTGAGCTC | | | 1879 |
| GGGACGAGAA | | | 1880 |
| GCCCAAGGAC | Human mRNA for actin-binding protein (filamin) (AB | X53416 | 1881 |
| CCACCCCCAC | Human serum constituent protein (MSE55) mRNA, comp | M88338 | 1882 |
| CAGCTCACTG | Homo sapiens mRNA for ribosomal protein L14, compl | D87735 | 1883 |
| TTTTCTGAAA | Human thioredoxin (TXN) mRNA, complete cds. | J04026 | 1884 |
| GGAGGGGGCT | Human mRNA for nuclear envelope protein lamin A pr | X03444 | 1885 |
| GCCAGCCCAG | Human unknown protein mRNA, partial | U31657 | 1886 |

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| | cds. | | |
| GAGGAGGGTG | | | 1887 |
| GTGGCACGTG | {Alu RNA transcript, clone NE461} [human, embryona | S42653 | 1888 |
| CTGGATCTGG | Human fetal brain glycogen phosphorylase B mRNA, c | U47025 | 1889 |
| TTCCACTAAC | Human plectin (PLEC1) mRNA, complete cds. | U53204 | 1890 |
| TGCAGCACGA | Human MHC class I (HLA-Cw8.1) mRNA exons 1-7, comp | M84174 | 1891 |
| TTGGTAATAT | Human dihydrofolate reductase gene. | J00140 | 1892 |
| TTGTAACTGG | | | 1893 |
| TTGTTGGAGA | H.sapiens mRNA for polyadenylate binding protein I | Z48501 | 1894 |
| AAGGACCTTT | | | 1895 |
| TTTAATACAT | | | 1896 |
| GCTAAGGAGA | Human ras-like protein mRNA, complete cds, clone T | M31467 | 1897 |
| CTGCACTTAC | Human mRNA for P1cdc47, complete cds. | D55716 | 1898 |
| TTGGATGAAG | | | 1899 |
| TGCTTTTAAC | Human mRNA for placental protein 5 (PP5), complete | D29992 | 1900 |
| ACAACGTCCA | Human mRNA for KIAA0230 gene, partial cds. | D86983 | 1901 |
| GTGGTGACCG | | | 1902 |
| GACGGCGCAG | Human platelet-derived endothelial cell growth fac | M63193 | 1903 |
| TTGGAGCTGA | | | 1904 |
| GTCTGACCCC | | | 1905 |
| AGGATGACCC | | | 1906 |
| TGCTGGGTGG | Homo sapiens folylpolyglutamate synthetase mRNA, c | M98045 | 1907 |
| TTGGCAACAT | | | 1908 |
| TGTGTGTTTG | | | 1909 |
| TTGGGCACTA | | | 1910 |
| GCCCCTCCGG | H.sapiens (xs99) mRNA, 344bp. | Z36851 | 1911 |
| GAGCCTTGGT | protein phosphatase type 1 catalytic subunit [huma | S57501 | 1912 |
| GGCTCCTGGC | H.sapiens mRNA for b4 integrin interactor. | Y11435 | 1913 |
| GGTCCAGTGT | Homo sapiens phosphoglycerate mutase (PGAM-B) mRNA | J04173 | 1914 |
| AGCCTTTGTT | Human mRNA for collagen binding protein 2, complet | D83174 | 1915 |
| TATATTTTAA | H.sapiens mRNA for transforming growth factor alph | X70340 | 1916 |

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|------------|--|--------|------|
| TCTGTCCTCA | Human mRNA for LCA-homolog. LAR protein (leukocyte | Y00815 | 1917 |
| TATATTTCCA | | | 1918 |
| TATATAGGTC | | | 1919 |
| TATAGTTGCT | Human mRNA for hCREM (cyclic AMP-responsive elemen | D14826 | 1920 |
| TTGCTTTTGT | Human ADP-ribosylation factor 4 (ARF4) mRNA, compl | M36341 | 1921 |
| TTGTAAAAGG | | | 1922 |
| TATAATTCAT | | | 1923 |
| AACAGTCAAA | | | 1924 |
| TATAAGGTGG | Human Gu protein mRNA, partial cds. | U41387 | 1925 |
| AAGTGGGTGC | Homo sapiens mRNA for CIRP, complete cds. | D78134 | 1926 |
| TATAAATAAT | | | 1927 |
| TAGGTCAGGA | | | 1928 |
| GAGAAACCCT | | | 1929 |
| CCCTGCTCCT | | | 1930 |
| GGAGCCCAGG | | | 1931 |
| CTCCCGGCGA | | | 1932 |
| CTCATCAGCT | Homo sapiens adenylyl cyclase-associated protein (| L12168 | 1933 |
| CTATGGCTTC | | | 1934 |
| CTACCCGGTA | Homo sapiens G protein-coupled receptor Edg-4 mRNA | AF0114 | 1935 |
| ACTACAGCAC | | | 1936 |
| TAGGAAACAC | | | 1937 |
| AGAAGGCTGC | protein kinase PRK1 [human, fetal brain, mRNA, 300 | S75546 | 1938 |
| TAGGTAGCTC | Homo sapiens spliced UHG RNA. | L36587 | 1939 |
| CCCCCTGCCC | | | 1940 |
| CAAGTGGCAA | | | 1941 |
| ATACTTTAAT | Human placenta anticoagulant protein PP4 mRNA, com | M19384 | 1942 |
| AGTTTCTTGT | | | 1943 |
| GTTGGATAGG | | | 1944 |
| CCTGTGATCC | | | 1945 |
| TCACCTGTAG | H.sapiens mRNA for kinase A anchor protein. | X97335 | 1946 |
| TATGCTGTTA | | | 1947 |
| TCAAATGCAA | Human mRNA for KIAA0156 gene, complete cds. | D63879 | 1948 |
| TCAACAGCCA | | | 1949 |
| TCACAAAGTG | | | 1950 |
| TCACAAGCCA | | | 1951 |
| CCGATCACCG | Human translational initiation factor 2 | M29536 | 1952 |

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| | beta subun | | |
| ATATAGGTCG | | | 1953 |
| TCAAAACTT | Human cell cycle control gene CDC2. | Y00272 | 1954 |
| TCACCTTAGG | | | 1955 |
| TCACTCCTGG | | | 1956 |
| TCAGAGGTGG | | | 1957 |
| ACAAATCCTT | Human FK506-binding protein (FKBP) mRNA, complete | M34539 | 1958 |
| AAATAAAAGC | thyrotropin receptor {3' region} [human, mRNA Part | S82807 | 1959 |
| TCAGGAGACG | | | 1960 |
| TCACCAAAC | | | 1961 |
| TATTTCCCTG | | | 1962 |
| TAGCCTCACT | | | 1963 |
| TATGGCCAGT | | | 1964 |
| TATGTATTTC | | | 1965 |
| GGCGGCTGCA | Homo sapiens excision repair protein (ERCC1) mRNA, | AF0019 | 1966 |
| GGCCTGCAGG | | | 1967 |
| CATAGAGCCA | | | 1968 |
| TATTTACTCT | | | 1969 |
| TATGCTTAGT | | | 1970 |
| GCACCTAGTG | Human acid finger protein mRNA, complete cds. | U09825 | 1971 |
| GCAACTTAGA | | | 1972 |
| TATTTGCTAC | | | 1973 |
| CTGGAGGCAC | | | 1974 |
| CTCTGTGTGG | Homo sapiens EB1 mRNA, complete cds. | U24166 | 1975 |
| TATTTTCTTC | | | 1976 |
| TATTGAAAGT | | | 1977 |
| CTTAAGGATT | | | 1978 |
| TAATGTGAGG | | | 1979 |
| ATTTTCCTTGA | | | 1980 |
| CACTCGTGTG | | | 1981 |
| TAATATGAGC | | | 1982 |
| CATTGCAGGA | | | 1983 |
| TAAGGCTTTT | | | 1984 |
| CCCAGGACAC | | | 1985 |
| TAAGCTCTCT | | | 1986 |
| TAAGCCTCCT | | | 1987 |
| TAAATTAATA | | | 1988 |
| TAAATATGAC | Homo sapiens mRNA for zinc finger protein FPM315, | D88827 | 1989 |
| TAAATAGGCA | Human mRNA for thrombospondin. | X04665 | 1990 |
| TAAATAAATA | Human mRNA for amyloid A4 precursor | Y00264 | 1991 |

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| | of Alzheimer's | | |
| GACCGAGGTG | | | 1992 |
| GCCCCAGCGA | | | 1993 |
| GTTGAAATAA | | | 1994 |
| GTTGATTTTA | | | 1995 |
| GTTGCTGGGG | | | 1996 |
| GGAGTGGGCT | | | 1997 |
| GTTGTTAACA | Homo sapiens heparan sulfate 3-O-sulfotransferase- | AF0193 | 1998 |
| TAAAGGCCAA | | | 1999 |
| GCGATTCCGG | | | 2000 |
| CTGGTCCTCC | | | 2001 |
| GTTTGATAAA | Human hypothetical protein A4 mRNA, complete cds. | U81556 | 2002 |
| GCAACCACGA | | | 2003 |
| TAAATCTTC | Human mRNA for calpastatin, complete cds. | D16217 | 2004 |
| TAAATGTGT | | | 2005 |
| TAAAGCACTT | | | 2006 |
| TACAGTTCAG | | | 2007 |
| GTTTCAGGAA | | | 2008 |
| TAGACCAGAT | Homo sapiens mRNA for KIAA0515 protein, partial cd | AB0110 | 2009 |
| TACAGGGGTC | | | 2010 |
| GTTGGGAGTC | | | 2011 |
| GTGACAGACA | Human nuclear factor NF45 mRNA, complete cds. | U10323 | 2012 |
| GTGAAGCTGA | | | 2013 |
| GTGAAACCCG | | | 2014 |
| TAACCCAACA | Human phosphoglucomutase 1 (PGM1) mRNA, complete c | M83088 | 2015 |
| TAGAAATGTT | | | 2016 |
| TACTGCCTCT | Homo sapiens centrosomal Nek2-associated protein 1 | AF0491 | 2017 |
| GCGAAGGTGG | | | 2018 |
| GCCGGCCGGA | | | 2019 |
| GCCGATCCTC | | | 2020 |
| GCCGACTCCG | | | 2021 |
| TAGATTCAAC | | | 2022 |
| GAGGAAGAAG | tumor rejection antigen/endoplasmic reticular heat | S74942 | 2023 |
| GTATTGGCCT | | | 2024 |
| TACCTTCATT | | | 2025 |
| TTCACCAGGG | H.sapiens mRNA for alpha-centractin. | X82206 | 2026 |
| AATTTCTATT | | | 2027 |
| AAAGTTCGTA | | | 2028 |

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|-------------|---|--------|------|
| GACTCTGCCT | | | 2029 |
| TTAGATAAGC | Human chaperonin protein (Tcp20) gene complete cds | L27706 | 2030 |
| TAACAGAAAG | Human DNA-binding protein (NF-E1) mRNA, complete c | M76541 | 2031 |
| TGTTGATTTT | Homo sapiens agrin precursor mRNA, partial cds. | AF0169 | 2032 |
| ACTCCCTCCT | | | 2033 |
| TGGAAGAAAC | | | 2034 |
| TGAACCCGCC | | | 2035 |
| TCTGTTTATC | Human 18 kDa Alu RNA binding protein mRNA, complet | U07857 | 2036 |
| TACTCTGCCC | | | 2037 |
| TCAGGCTGTT | H.sapiens mRNA for beta-centractin (PC3). | X82207 | 2038 |
| TATTCCCCAC | | | 2039 |
| GAAGAACAAG | | | 2040 |
| TCCTCGGGCA | | | 2041 |
| AGCCCGCCGC | Homo sapiens tumor-suppressing subchromosomal tran | AF0199 | 2042 |
| ATTGGACACA | H.sapiens mRNA for nucleoside- diphosphate kinase. | Y07604 | 2043 |
| CAGTGGGTGT | | | 2044 |
| CCAGGCTGCG | Human integrin beta-5 subunit mRNA, complete cds. | J05633 | 2045 |
| TGCAGTGA CT | H.sapiens mRNA for 37 kDa LIM domain protein. | X93510 | 2046 |
| CTTTCCCCTT | | | 2047 |
| GAGGATGGTG | Human mRNA for C3G protein, complete cds. | D21239 | 2048 |
| GATTCAAGTC | Homo sapiens mRNA for mitochondrial ribosomal prot | Y11681 | 2049 |
| TGATTTTCAC | | | 2050 |
| GCCCCCCCGT | | | 2051 |
| GGAACGGATG | | | 2052 |
| GGATTGTCTG | Human small nuclear ribonucleoprotein particle SmB | M34081 | 2053 |
| TGATTTGCT | | | 2054 |
| TCAGGGCTGA | | | 2055 |
| AACCCAAACT | | | 2056 |
| ATCACAGGCC | | | 2057 |
| TGAAGTTATA | Human mRNA for fibronectin receptor beta subunit. | X07979 | 2058 |
| ACCCACAGTG | | | 2059 |
| ACCAAGGAGG | Human RNA polymerase II 23kD subunit (POLR2) mRNA, | J04965 | 2060 |
| TGAATTCTAC | | | 2061 |

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|------------|--|--------|------|
| GTGTTCTTGG | Homo sapiens phosphatidic acid phosphatase type 2 | AF0560 | 2062 |
| AAGCGGGACC | H.sapiens TE2 mRNA for ARD-1 N-acetyltransferase h | X77588 | 2063 |
| TAAGAAAAGG | | | 2064 |
| TGAGGAGCTC | | | 2065 |
| TGGTCTGGAG | Human mRNA for KIAA0216 gene, complete cds. | D86970 | 2066 |
| TGAGTGGTAG | Human mRNA for nuclear envelope protein lamin C pr | X03445 | 2067 |
| TGATCCTTGT | | | 2068 |
| TGATGGCTCC | Homo sapiens arylsulphatase A mRNA, complete cds. | X52151 | 2069 |
| TGCCAGGACT | Human nucleotide-binding protein mRNA, complete cd | U01833 | 2070 |
| TGAGCACTCG | | | 2071 |
| AAAATATTTT | Human mRNA for alpha-actinin, partial cds. | X55187 | 2072 |
| ACTACCTTCA | Homo sapiens px19 protein pseudogene mRNA, partial | U94779 | 2073 |
| CAGCCCAACC | Homo sapiens eukaryotic translation initiation fac | AF0208 | 2074 |
| TGCTGTGAAA | | | 2075 |
| TGCTGTGACC | | | 2076 |
| ACCGCTTGTT | Human type 3 inositol 1,4,5-trisphosphate receptor | U01062 | 2077 |
| CAGTTGGTTG | Human RNA fragment from patients with Crohn's dise | U55217 | 2078 |
| AAGCCCAGGC | | | 2079 |
| TGCTGGAATT | | | 2080 |
| TTTTCTGCTG | | | 2081 |
| TGCTTGTGGT | | | 2082 |
| TTCACTGCCG | Human fetus brain mRNA for vacuolar ATPase, comple | D49400 | 2083 |
| TGCTTTCTTA | | | 2084 |
| TGCTTTGCTT | Human mRNA for KIAA0207 gene, complete cds. | D86962 | 2085 |
| GGGCCCAGGA | | | 2086 |
| AAGGAATCGG | | | 2087 |
| TGCCTGGAAA | Homo sapiens APECED mRNA for AIRE-3, complete cds. | AB0066 | 2088 |
| TGAAGACAAC | | | 2089 |
| TTTCCACTTA | Human SIP-1 mRNA, complete cds. | U82108 | 2090 |
| ITGCCGGTTA | | | 2091 |
| TGCTGCCCTG | Human mRNA for B-myb gene. | X13293 | 2092 |
| TAGAAAAATA | Human transactivator protein (CREB) mRNA, complete | M27691 | 2093 |

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|-------------|--|--------|------|
| CAGCTGTAGT | Human mRNA for KIAA0174 gene, complete cds. | D79996 | 2094 |
| GTCTCCTAAT | | | 2095 |
| TGCATCAGAA | | | 2096 |
| GGGTGTGTAT | Homo sapiens angio-associated migratory cell prote | M95627 | 2097 |
| TGCCTTTAAC | | | 2098 |
| GCCGCCATCA | Human mRNA for protein disulfide isomerase-related | D49489 | 2099 |
| GCCAGACACC | | | 2100 |
| TGCGCGCCCT | | | 2101 |
| TGCTGCTGCT | Homo sapiens GT219 mRNA. | L38936 | 2102 |
| G TTCAGCTGT | Homo sapiens porin (por) mRNA, complete cds and tr | L08666 | 2103 |
| CAGCGCTTTG | | | 2104 |
| TCTACAGCTG | Human FE65-like protein (hFE65L) mRNA, partial cds | U62325 | 2105 |
| TCCTCAACCT | | | 2106 |
| TCCTCTGTGC | | | 2107 |
| TCCTGGGGCA | | | 2108 |
| CGGAGTCCAT | Human mRNA for Diff6, H5, CDC10 homologue, complet | D28540 | 2109 |
| TCCGTGTATA | | | 2110 |
| CCCCAGTCGG | Human protein tyrosine kinase mRNA, complete cds. | M59371 | 2111 |
| TCCGTATTAA | | | 2112 |
| ATGTGCGTGG | Human SNC19 mRNA sequence. | U20428 | 2113 |
| TCGCCAGCCC | Homo sapiens DGS-I mRNA, 3' end. | L77566 | 2114 |
| TCGGCTTTAT | | | 2115 |
| TCGGGCCGCG | | | 2116 |
| ACCACACCCT | Human fra-1 mRNA. | X16707 | 2117 |
| ATGTACCTGA | Human XMP mRNA, complete cds. | U52100 | 2118 |
| TCGAAAGCCC | | | 2119 |
| TCCAGAACGC | | | 2120 |
| GGGCCTGGGG | | | 2121 |
| TTAATAAAAG | | | 2122 |
| TGTTACTGCT | Human HepG2 3' region cDNA, clone hmd3h09. | D16927 | 2123 |
| TCATCAGGAC | | | 2124 |
| TCATTTTCAGA | Human erythroblastosis virus oncogene homolog 2 (e | J04102 | 2125 |
| TCCTAATCCC | | | 2126 |
| TCCACGTACA | | | 2127 |
| AACAGAAGCA | | | 2128 |
| TCCAGAGAAG | | | 2129 |
| TCCATTTTCT | | | 2130 |

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| TCCCACCCAC | | | 2131 |
| GGGCTGCGTC | | | 2132 |
| TCCCGTAATC | | | 2133 |
| GGAGGTAGGG | Human transmembrane receptor precursor (PTK7) mRNA | U40271 | 2134 |
| TCCAAACCAC | | | 2135 |
| TCTTTCCTT | | | 2136 |
| TCGTTATGCA | | | 2137 |
| TCTCTTCCC | | | 2138 |
| GGACTGGCCC | | | 2139 |
| TCTGATATGG | | | 2140 |
| TCTGCAAGAA | | | 2141 |
| GGGGTCTGGG | | | 2142 |
| TCTTCCCTCA | | | 2143 |
| GTAGCGCACG | | | 2144 |
| TCTTTCTACC | | | 2145 |
| TCTTTGTCAT | | | 2146 |
| TGAAAGAAGT | | | 2147 |
| CATCTAAACT | Human mRNA for KIAA0038 gene, partial cds. | D26068 | 2148 |
| CAGGATCCAG | Human progesterone receptor-associated p48 protein | U28918 | 2149 |
| TCAGTTATCT | | | 2150 |
| GACCCACTAC | Human lymphocyte activation antigen 4F2 large subu | J03569 | 2151 |
| TCTCCTTCAT | | | 2152 |
| TCTATTGGTG | | | 2153 |
| TCTCCAAGGA | | | 2154 |
| TTCTTCTCGT | H.sapiens mRNA for SMT3A protein. | X99584 | 2155 |
| TGTTTGGGGG | | | 2156 |
| TCTCCATCAC | | | 2157 |
| GGGCAGGCGT | Human transcription factor ETR101 mRNA, complete c | M62831 | 2158 |
| TGAGTCCCTG | Homo sapiens Pig12 (PIG12) mRNA, complete cds. | AF0103 | 2159 |
| CACCGGACAC | | | 2160 |
| TCCAGCCCCT | | | 2161 |
| TCATAGAAAC | Human mRNA for KIAA0098 gene, partial cds. | D43950 | 2162 |
| TATTTATTCC | Human mRNA for Src-like adapter protein, complete | D89077 | 2163 |
| TAAAGTGTCT | | | 2164 |
| GTGGTGGGTG | Human RACH1 (RACH1) mRNA, complete cds. | U35735 | 2165 |
| TCTCTTGACA | | | 2166 |
| TGCGTTTGCT | | | 2167 |

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| AGGAACCAGA | Human phosphatase 2A inhibitor I2PP2A mRNA, comple | U51924 | 2168 |
| TCTGTGACTT | | | 2169 |
| AGCAATTTCA | | | 2170 |
| AGCACAGAGG | | | 2171 |
| AGCAGAGGCT | Human epidermoid carcinoma mRNA for ubiquitin-conj | D83004 | 2172 |
| AGCAGCCTTT | Human mRNA for p97 homologous protein, partial cds | D86549 | 2173 |
| AGCCACTGTA | | | 2174 |
| TCTGGGAGAA | | | 2175 |
| AGCCCCTACA | | | 2176 |
| TCTGGACTCG | Homo sapiens mRNA for putative ABC transporter, pa | AJ0050 | 2177 |
| AGCCGCAAAC | Human mRNA for proteasome subunit p27, complete cd | AB0031 | 2178 |
| AGCCGGGCTT | | | 2179 |
| AGCCTGACTG | H.sapiens mRNA for 2.19 gene. | X87193 | 2180 |
| AGCCTGGAGA | | | 2181 |
| TCGGAGCTGT | | | 2182 |
| AGGCAGGAGG | | | 2183 |
| TGACTGGCCA | | | 2184 |
| AGGCTGCGAC | | | 2185 |
| TCTAAGCCCC | | | 2186 |
| AGGCTATTGG | | | 2187 |
| AGGCGCTTAG | | | 2188 |
| AGCCTGTGCT | Human mRNA for leukotriene b4 receptor, complete c | D89079 | 2189 |
| TCTATCTCAG | | | 2190 |
| AGCTCTGGAA | | | 2191 |
| AGGCAACTGG | | | 2192 |
| AGGATAACTT | | | 2193 |
| AGGAGGGTGG | Human lamin B mRNA, complete cds. | M34458 | 2194 |
| TCTCTGCCTC | | | 2195 |
| AGGAGAGAAG | | | 2196 |
| TCTTTTATTA | | | 2197 |
| AGGCCCCAGG | | | 2198 |
| ACCCGCGAGG | | | 2199 |
| TCTTCAGTAG | | | 2200 |
| ACCTGGCCTG | | | 2201 |
| TGAAGTCACT | | | 2202 |
| ACCTACGATG | Human phorbolin I mRNA, partial cds. | U03891 | 2203 |
| TGAATGTGGA | | | 2204 |
| ACGTAATTAG | | | 2205 |
| ACCCTCCTGT | | | 2206 |
| ACGTCGTCGA | | | 2207 |

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| ACCCGCCTGT | | | 2208 |
| ACCCAGTTGT | | | 2209 |
| ACCCAATCAG | | | 2210 |
| ACCATTGTGT | | | 2211 |
| ACCAGGTCCA | | | 2212 |
| CAGCCCCGCC | | | 2213 |
| TGACCACCTA | | | 2214 |
| ACTGTGGTAG | | | 2215 |
| AGGTCAGGAA | | | 2216 |
| AGACACCTGT | | | 2217 |
| TGAAAGTAAA | | | 2218 |
| AGAACCTTAA | | | 2219 |
| AGAAAATGTG | | | 2220 |
| ACGGAAGTTT | | | 2221 |
| ACTTACCTGT | | | 2222 |
| AGAGCTCCAT | | | 2223 |
| ACTGGTGGTC | | | 2224 |
| ACTGCTGTCT | | | 2225 |
| ACTGCCACAG | | | 2226 |
| ACTGAGGAAC | | | 2227 |
| ACTCAGCCCC | | | 2228 |
| ACTATTCCAT | | | 2229 |
| ACTTGCGAAT | | | 2230 |
| CACCTAAATG | | | 2231 |
| ATTTATCCTA | | | 2232 |
| TCCCTCTCAG | | | 2233 |
| ATTTGGGACC | | | 2234 |
| ATTTCTCTT | | | 2235 |
| ATTTCTCATT | | | 2236 |
| ATTTTTTACA | | | 2237 |
| CAAAGTGCTT | Human cAMP-dependent protein kinase regulatory sub | M18468 | 2238 |
| TCCATTAAGC | | | 2239 |
| CAAAGGCCCT | | | 2240 |
| TCCAGTTCTG | | | 2241 |
| TCCAGGCTCT | | | 2242 |
| TCCACCTGTC | | | 2243 |
| CAATTACCTG | | | 2244 |
| AGGCTGGGGG | | | 2245 |
| CACTGCAAGG | | | 2246 |
| AAAGAAAGCC | | | 2247 |
| CAGCAAAAAA | pyruvate carboxylase [human, kidney, mRNA, 4017 nt | S72370 | 2248 |
| CAGATATATA | Human cDNA for uracil-DNA glycosylase. | X15653 | 2249 |
| CAGAGCCTGC | | | 2250 |

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| CAGAGACCAA | | | 2251 |
| CACAGGCCTG | Human zinc finger protein zfp2 (zf2) mRNA, partial | U71598 | 2252 |
| TCACCATAGA | | | 2253 |
| TCAGACGCCA | | | 2254 |
| CACTCCAATA | | | 2255 |
| CACTCACACC | Human SR31747 binding protein 1 mRNA, complete cds | U79528 | 2256 |
| CACGACTGTT | | | 2257 |
| TCACTCTTTG | | | 2258 |
| CACCTCATCC | | | 2259 |
| TCCCTGAGCA | Human mRNA for KIAA0056 gene, partial cds. | D29954 | 2260 |
| CACTGGAAGG | | | 2261 |
| AGTTTGAGGC | Homo sapiens hCAP1b mRNA for mRNA capping enzyme, | AB0121 | 2262 |
| ATTTAGGCAA | | | 2263 |
| TCGATATTTG | | | 2264 |
| ATCCTGTAGG | | | 2265 |
| TCGCCCAGGC | | | 2266 |
| TCGCGCAATA | | | 2267 |
| ATGAACAGCG | Human transcription factor RTEF-1 (RTEF1) mRNA, co | U63824 | 2268 |
| ATATAAAAAT | | | 2269 |
| TCCTTTTCCT | | | 2270 |
| AGTTAGCAGT | | | 2271 |
| AGTGTGATAC | | | 2272 |
| AGTGGCTGTG | | | 2273 |
| AGTGGAGGTG | | | 2274 |
| AGTAATCATC | Human mRNA for proteasome inhibitor hPI31 subunit, | D88378 | 2275 |
| AGGTGGTTAG | | | 2276 |
| ATATGGGGTG | | | 2277 |
| ATGGTGAGCG | | | 2278 |
| ACACTTACAA | Homo sapiens UEV1Bs (UBE2V) mRNA, alternatively sp | U97280 | 2279 |
| ATTGTAAACT | | | 2280 |
| ATTGCCCGTG | | | 2281 |
| TCCGCGTACA | | | 2282 |
| ATGTTTAATT | | | 2283 |
| ATGAAACTTC | | | 2284 |
| ATGGTGGGTG | | | 2285 |
| ATTGTGCTTG | | | 2286 |
| ATGGCTGCTG | | | 2287 |
| TCCTTATTAA | | | 2288 |
| ATGGCACCCAC | Human mRNA for interleukin-2 | X01057 | 2289 |

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| | receptor. | | |
| TCCTTGAATA | | | 2290 |
| ATGCTTTTAT | | | 2291 |
| ATGACTGCTG | | | 2292 |
| TCCTGCATTT | | | 2293 |
| TTCCCCCTTC | | | 2294 |
| TTGTATTCCA | H.sapiens mRNA for alpha 4 protein. | Y08915 | 2295 |
| TTGGTGCTTG | | | 2296 |
| TTGGGGTTTA | | | 2297 |
| TTGGGCCAGG | | | 2298 |
| TTGGCTGTCT | | | 2299 |
| TTGGCCAGGT | | | 2300 |
| TTGGCCAGGG | | | 2301 |
| TTGGCAAGCG | | | 2302 |
| TTGCACAACC | Human EST clone NIB1543 mariner transposon Hsmar1 | U80776 | 2303 |
| TTGAGGGGGT | | | 2304 |
| TTCTTTTGCT | | | 2305 |
| TTCTAGCAA | | | 2306 |
| TTCCCTGCAA | Human precerebellin and cerebellin mRNA, complete | M58583 | 2307 |
| TGTTCGGTTG | | | 2308 |
| TTAAGAAGCC | | | 2309 |
| ACATCAAAAT | Homo sapiens spermidine aminopropyltransferase mRN | AD0015 | 2310 |
| TGTTTCCCAA | Human mRNA for KIAA0011 gene, complete cds. | D13636 | 2311 |
| TGTTTGGAAC | Human TNF-alpha converting enzyme mRNA, complete c | U86755 | 2312 |
| TTTTTTTAAA | | | 2313 |
| TGTTTTCAGG | | | 2314 |
| TTCCCCTTCC | | | 2315 |
| TGTTTTGAAT | | | 2316 |
| TTCCCCGTAC | | | 2317 |
| TTACAATTTA | | | 2318 |
| TTACAGTCTT | | | 2319 |
| TTACTGGGTT | | | 2320 |
| TTCCAGACTT | | | 2321 |
| TTCCAGGTTT | | | 2322 |
| TTGTTCTTTG | Human phosphatase 2A mRNA, complete cds. | J03804 | 2323 |
| CTAAGACTTC | | | 2324 |
| AAAAAAAAGA | | | 2325 |
| TTGTCCTCAG | | | 2326 |
| TTTTCGGCAA | Homo sapiens proline-rich Gla protein 2 (PRGP2) mR | AF0092 | 2327 |

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| TTTTCTTCAC | Human cytosolic serine hydroxymethyltransferase (S | L11931 | 2328 |
| TTTTGTAATT | Human mRNA for KIAA0091 gene, complete cds. | D42053 | 2329 |
| TTTTGTATAT | | | 2330 |
| TTTTATTAAA | | | 2331 |
| AAAAAAAAAAG | | | 2332 |
| TTTTATGACC | Homo sapiens clone 23689 mRNA, complete cds. | AF0352 | 2333 |
| AAAACATCTC | | | 2334 |
| AAAAGCAGGA | | | 2335 |
| AAAATAAAAA | Human mRNA for protoporphyrinogen oxidase, complet | D38537 | 2336 |
| AAACAGAGCT | | | 2337 |
| AAACATTACC | | | 2338 |
| ATTTTATATC | Homo sapiens (clone S31i125) mRNA, 3' end of cds. | L40397 | 2339 |
| TTTTGTTTTG | | | 2340 |
| TTTCTGGAGG | Homo sapiens mRNA for KIAA0545 protein, partial cd | AB0111 | 2341 |
| TGTGGCCTGC | Human glucose-6-phosphate dehydrogenase (G6PD) mRN | M35604 | 2342 |
| TTTAATTTGT | | | 2343 |
| TTTATTTAAG | Human mRNA for HHR23A protein, complete cds. | D21235 | 2344 |
| TTTCACCCCT | | | 2345 |
| TTTCCAGGGG | | | 2346 |
| TTTTCAAGAA | | | 2347 |
| TTTCTCGTCG | Homo sapiens guanine nucleotide binding protein al | AF0114 | 2348 |
| TTGTCCTTTT | | | 2349 |
| TTTGAGCTGG | | | 2350 |
| TTTGATAAAT | | | 2351 |
| TTTGCACTTG | H.sapiens Wee1 hu gene. | X62048 | 2352 |
| TTTGGAATGT | | | 2353 |
| TTTGTTAATT | Human hnRNP H mRNA, complete cds. | L22009 | 2354 |
| TTTGTTGTTG | | | 2355 |
| TTTCCTTGTG | | | 2356 |
| AAGTTCTGCG | Human replication protein A 32-kDa subunit mRNA, c | J05249 | 2357 |
| AAGACATTCT | | | 2358 |
| AAGAGACACA | | | 2359 |
| AAGATGAGGG | | | 2360 |
| TGCACGCACA | | | 2361 |
| AAGCAGGAGG | Homo sapiens mad protein homolog | U68019 | 2362 |

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| | (hMAD-3) mRNA, co | | |
| AAGCCAGGGG | | | 2363 |
| AAGCTGTTGT | H.sapiens mRNA for DNA (cytosin-5)-methyltransfera | X63692 | 2364 |
| TGATTCATTT | | | 2365 |
| TGATGTTTGC | | | 2366 |
| AAGGATTCAC | | | 2367 |
| AAGGCAGAAG | | | 2368 |
| AAGGTGGAAG | | | 2369 |
| TGATGAGTGC | | | 2370 |
| TGTTCTTTAG | H.sapiens mRNA for protein-tyrosine-phosphatase (t | X93920 | 2371 |
| AATGGAGACT | Human mRNA for 19kD protein of signal recognition | X12791 | 2372 |
| ACACAGTTTT | Human HepG2 3' region Mbol cDNA, clone hmd3e02m3. | D17205 | 2373 |
| ACAAGCATTT | Human CDK4-inhibitor (p16-INK4) mRNA, complete cds | L27211 | 2374 |
| ACAAAGGGCC | Homo sapiens KIAA0397 mRNA, complete cds. | AB0078 | 2375 |
| TGAGATTTCT | | | 2376 |
| AATTTGAGAA | | | 2377 |
| AAGTCCCAGG | | | 2378 |
| AATTAATTGT | | | 2379 |
| TGATGACTGT | | | 2380 |
| AATGAACAAT | Human ninjurin1 mRNA, complete cds. | U72661 | 2381 |
| TGAGCGTGGG | | | 2382 |
| AATATTTCAA | Homo sapiens cytoplasmic phosphotyrosyl protein ph | M83654 | 2383 |
| TGAGTCTGGC | | | 2384 |
| TGATCTGTTG | | | 2385 |
| AACCCGGGAA | | | 2386 |
| AATTCTGTAA | | | 2387 |
| TGGTCCAGCG | Human CD14 mRNA for myelid cell-specific leucine-r | X13334 | 2388 |
| AAGAAGGGAG | | | 2389 |
| TGGATCATCA | | | 2390 |
| TGGATCCCAG | Human TFIIID subunit p22 mRNA, complete cds. | D50544 | 2391 |
| TGGATCCTAG | | | 2392 |
| TGGCAATGGC | | | 2393 |
| TGGAACCTTG | | | 2394 |
| TGGTAGAGCG | | | 2395 |
| TGCTAACTGC | | | 2396 |
| TGGTCCCTCT | H.sapiens sds22-like mRNA. | Z50749 | 2397 |
| TGTAAATGG | | | 2398 |

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| TGTCACACAC | | | 2399 |
| TGTCCTCCCC | | | 2400 |
| TGTCTTAAGG | | | 2401 |
| TGTGCTGTGC | Human UDP glucose:glycogen 4-alpha-D-glycosyltransf | U32573 | 2402 |
| TGGCTGTGAC | Human mRNA for KIAA0110 gene, complete cds. | D14811 | 2403 |
| AAACCAGAGG | Human lymphoid-restricted membrane protein (Jaw1) | U10485 | 2404 |
| CAGCTTGACG | | | 2405 |
| TGCCAAAAAA | | | 2406 |
| TGCCCCACTCA | | | 2407 |
| TGCCTCCCAT | Human eukaryotic initiation factor 2B-epsilon mRNA | U23028 | 2408 |
| AAAGGAAAGT | | | 2409 |
| TGGAGACTGG | Homo sapiens mRNA for Dnm1p/Vps1p-like protein, co | AB0069 | 2410 |
| AAACCTCTCA | | | 2411 |
| TGCAGGTGGC | | | 2412 |
| AAACATTCTC | | | 2413 |
| AAAATTATTA | | | 2414 |
| TGCCTGTGGT | | | 2415 |
| AAAACAAAAA | | | 2416 |
| AAAAATGTGT | | | 2417 |
| TGCGGCTGGT | H.sapiens mRNA for dynactin. | X98801 | 2418 |
| AAACTGTGAA | | | 2419 |
| GCCCTGACCT | | | 2420 |
| GTGGCTGAGC | | | 2421 |
| GCAGTTCAAG | | | 2422 |
| GCAATTGGTA | | | 2423 |
| GCCAAGACAC | | | 2424 |
| GTGGAGGGGC | Human protein-tyrosine phosphatase mRNA, complete | U27193 | 2425 |
| GCCAATGTGG | Homo sapiens mRNA for putative glucose 6-phosphate | Y15409 | 2426 |
| GCCAGCTCAG | | | 2427 |
| GCCAGGGCGC | | | 2428 |
| GCCAGTGGCC | | | 2429 |
| GCCCCCTTCC | | | 2430 |
| GTGCTCAAAC | Human mRNA for KIAA0346 gene, partial cds. | AB0023 | 2431 |
| GCCCGCAGTG | | | 2432 |
| GTGCAGGCTC | Homo sapiens peptide transporter (TAP1) mRNA, comp | L21208 | 2433 |
| GTGACTGGCA | | | 2434 |
| GCCTCAGGGA | | | 2435 |

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| GAGAAACCCA | | | 2436 |
| GTGATATCCA | | | 2437 |
| GCGAACCGTC | | | 2438 |
| GCGAAAAGCT | | | 2439 |
| GTGATGCTGG | | | 2440 |
| GCCCGTGTCC | | | 2441 |
| GCCTGATTTT | Human kidney mRNA for putative membrane protein wi | D82060 | 2442 |
| GCCCTCACAG | Human fragile X mental retardation syndrome relate | U31501 | 2443 |
| GTGATTTGTT | | | 2444 |
| GCCGGTTGGG | | | 2445 |
| GCCGCCTGTG | | | 2446 |
| GCCGCCTGCC | Human IMP dehydrogenase type 1 mRNA complete cds. | J05272 | 2447 |
| GTGCAGAGAG | | | 2448 |
| GCACTTCAAG | | | 2449 |
| GCCTTGGGTG | Human mRNA for leukaemia inhibitory factor (LIF/HL | X13967 | 2450 |
| GTTTAGTCTC | | | 2451 |
| GCAGCCCGCG | | | 2452 |
| GTTCCAAGCA | | | 2453 |
| GAGTCTTCTG | | | 2454 |
| GTTCTGGGCG | | | 2455 |
| GAGGTTCTTC | Human hydroxymethylglutaryl-CoA lyase mRNA, comple | L07033 | 2456 |
| GATAATTTTT | | | 2457 |
| GTTGGTGGCA | | | 2458 |
| GATCTCACTG | | | 2459 |
| GAGGAACCAG | | | 2460 |
| GAGCTGCAGG | | | 2461 |
| GAGCGCAGCG | Human cleavage and polyadenylation specificity fac | U37012 | 2462 |
| GAGCCAACCC | | | 2463 |
| GAGACCCTGG | Homo sapiens clone 24666 sec6 homolog mRNA, partia | AF0550 | 2464 |
| CAGCAGCGGC | | | 2465 |
| GAGGGTCTTG | | | 2466 |
| GCAACAAATC | | | 2467 |
| GCGGAAACTG | | | 2468 |
| GTGGGGAGGA | | | 2469 |
| GTGGGGCTAT | | | 2470 |
| GTGGGTCAGC | | | 2471 |
| GCACACTAGC | | | 2472 |
| GAGTTAGGCA | Homo sapiens clone 1400 unknown protein mRNA, part | AF0207 | 2473 |

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| GCAACTTGGA | Homo sapiens SH3-containing adaptor molecule-1 mRN | AF0372 | 2474 |
| GTGGCTGCTG | | | 2475 |
| GCAAAACTCT | | | 2476 |
| GATGTGTGCT | | | 2477 |
| GATGTGGAGA | | | 2478 |
| GATGTAGTAT | | | 2479 |
| GTGTTCTCC | | | 2480 |
| GATGCATATA | | | 2481 |
| GCAAGGCAGA | | | 2482 |
| GGTATGACAT | Human fatty acid amide hydrolase mRNA, complete cd | U82535 | 2483 |
| GTATCTTCAA | | | 2484 |
| GTAGGGGCCT | | | 2485 |
| GGATGAGTCT | Human anti-c-erbB-2 immunoglobulin light chain V m | U38346 | 2486 |
| GGCAGCCTGG | Human ERPROT 213-21 mRNA, complete cds. | U94836 | 2487 |
| GGCAGGCACC | | | 2488 |
| GGCAGGCTGT | Homo sapiens cyclophilin-33A (CYP-33) mRNA, comple | AF0423 | 2489 |
| GGCATAATAG | | | 2490 |
| GTAGCAGGGC | | | 2491 |
| GGCATTGTTC | H.sapiens mRNA for RNA polymerase II subunit hRPB1 | Z49199 | 2492 |
| GTACATCCTT | Human arfaptin 2, putative target protein of ADP-r | U52522 | 2493 |
| GGTTGAGTGT | | | 2494 |
| GGCCTTCCTT | | | 2495 |
| GGTGAAAGAG | | | 2496 |
| GCGACAGTCC | | | 2497 |
| GGGACAGGCA | | | 2498 |
| GGGGGGGTCT | Homo sapiens protein phosphatase 2A B56-gamma1 (PP | L42375 | 2499 |
| GGGCGGGTCC | Human sky mRNA for Sky, complete cds. | D17517 | 2500 |
| GGGGGTGGAT | H.sapiens mRNA for FAST kinase. | X86779 | 2501 |
| GGGCCTTTTC | | | 2502 |
| GGGCAGGGGC | | | 2503 |
| GGTCTGTCTC | | | 2504 |
| GGGAGACCCC | | | 2505 |
| GGTCAGGGTG | | | 2506 |
| GGGAAGATGA | Human heat shock protein 27 (HSP27) mRNA, complete | U15590 | 2507 |
| GGGTGGGGGC | | | 2508 |
| GGCTTAAAAA | | | 2509 |

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| GGCTGGGTTT | Human homeobox gene, complete cds. | M60721 | 2510 |
| GGCTGGGGTC | | | 2511 |
| GGAATATGCA | | | 2512 |
| GGGCAAGCCA | Human estrogen receptor-related protein (hERRa1) m | L38487 | 2513 |
| GCTAGGCCGG | | | 2514 |
| GTATGACCAG | | | 2515 |
| GCTGCCCCTG | | | 2516 |
| GCCTGCTCC | | | 2517 |
| GTCTTTAGGA | | | 2518 |
| GTGAAACCAC | | | 2519 |
| GCTGGCTGGG | | | 2520 |
| GTGAAACCAT | | | 2521 |
| GTCCCAAAT | H. sapiens cDNA for RFG. | X77548 | 2522 |
| GTGAAACCGT | | | 2523 |
| GCTACAGGTA | | | 2524 |
| GTGACAGCCA | | | 2525 |
| GCGTGGCTCA | | | 2526 |
| GTGACGGGCG | | | 2527 |
| GCGGCCTCAG | | | 2528 |
| GCTCCCTCCT | | | 2529 |
| GCTTCTGCCA | | | 2530 |
| GAGAAAAAGT | | | 2531 |
| GGAAGTTAAG | | | 2532 |
| GGAAGTCTGT | | | 2533 |
| GGAAAGTGAC | | | 2534 |
| GGAAACCCCA | Homo sapiens dishevelled 3 (DVL3) mRNA, complete c | AF0060 | 2535 |
| GCTGCCTGCC | | | 2536 |
| GCTTGAATTA | | | 2537 |
| GTATGTCCAT | | | 2538 |
| GTATTGGAGA | | | 2539 |
| GCTTCCTCTG | | | 2540 |
| GTATTTGTGG | | | 2541 |
| GCTTATGCTT | Human mRNA for uKATP-1, complete cds. | D50312 | 2542 |
| GCTTAATTGT | | | 2543 |
| GTCAACTGCT | | | 2544 |
| GCTTGGCTCC | | | 2545 |
| CCTGGCCCTA | | | 2546 |
| CCGAATACCG | | | 2547 |
| CCGCCTCCGG | Human lupus autoantigen (small nuclear ribonuclepo | J04615 | 2548 |
| CCGGAATGTG | | | 2549 |
| CCGTGAAAAA | | | 2550 |
| TACTTGGTCT | | | 2551 |

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| CCTAAGGGAG | Homo sapiens transcription factor SL1 mRNA, comple | L39059 | 2552 |
| TACTTGCTAT | | | 2553 |
| CCTATAGTCC | Human mRNA for D-aspartate oxidase, complete cds. | D89858 | 2554 |
| CCTATTAAAC | | | 2555 |
| CCTCAGCCCT | Human tyrosine phosphatase mRNA, complete cds. | M77273 | 2556 |
| CCTCCCAGCT | | | 2557 |
| TACTGGTGTA | | | 2558 |
| TACTGATTAC | | | 2559 |
| CGGATCCAGT | | | 2560 |
| CCTTTGAAAC | | | 2561 |
| GTTTATGTTC | | | 2562 |
| CGCCCGGAAC | | | 2563 |
| CGCCAAGCTG | | | 2564 |
| CGCAAAAAAA | | | 2565 |
| CGACTGTAAT | | | 2566 |
| CCTGATGAAG | | | 2567 |
| CCTTTGTAAA | | | 2568 |
| CCTGCCAAAG | | | 2569 |
| TACGGGGATC | | | 2570 |
| CCTTGGGCCT | | | 2571 |
| CCTTGCTTTT | | | 2572 |
| CCTGTCTGCA | | | 2573 |
| CCTGGCTCAA | | | 2574 |
| TAGTCTGGAG | Human CDP-diacylglycerol synthase mRNA, complete c | U65887 | 2575 |
| CGAATAAAAT | | | 2576 |
| CAGGTCATAC | | | 2577 |
| CCCTGGGGTT | | | 2578 |
| CATTCTCCTA | | | 2579 |
| CATCCCCACC | | | 2580 |
| CATCAGCACT | | | 2581 |
| CATCACACTC | | | 2582 |
| CATTTTATTT | | | 2583 |
| CAGGTGGTGA | | | 2584 |
| TATGGGGTCA | | | 2585 |
| CAGGGGAAGG | | | 2586 |
| CAGGGATCTG | | | 2587 |
| TCAAGTTCAC | | | 2588 |
| CAGGCTTTTT | | | 2589 |
| TCAATGGACA | | | 2590 |
| TCACAATAGG | Homo sapiens expressed pseudo TCTA mRNA at t(1;3) | L41143 | 2591 |
| CAGTTCCATA | | | 2592 |

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|-------------|--|--------|------|
| CCCAGGAGGA | | | 2593 |
| CGGCCACAGA | Human HepG2 partial cDNA, clone hmd2c12m5. | D16990 | 2594 |
| TATAAAATTT | Human fumarase precursor (FH) mRNA, nuclear gene e | U59309 | 2595 |
| TATCTTCTAA | Human hypoxanthine phosphoribosyltransferase (HPRT | M31642 | 2596 |
| CCCCTTTGCA | | | 2597 |
| CCCCAAGCTA | | | 2598 |
| TATGTGCTGT | | | 2599 |
| CCCAGTGGCC | | | 2600 |
| TAGGCAACAC | | | 2601 |
| CCATTGTACT | | | 2602 |
| CCAGGCACTG | | | 2603 |
| CCACTTCTGG | | | 2604 |
| TATGGCTACA | | | 2605 |
| CCACAATCCT | | | 2606 |
| CCAAGACTTC | | | 2607 |
| CCCATTGTCC | | | 2608 |
| GAAAAGGTTA | | | 2609 |
| CTTACTCGGG | | | 2610 |
| CTTATAATCC | | | 2611 |
| CTTCCAGTAA | | | 2612 |
| CTTCGCGATG | | | 2613 |
| CTTCGGGCTG | | | 2614 |
| TAAATAAAGC | | | 2615 |
| CTTGTAACAG | Human laminin B1 chain mRNA, complete cds. | M61916 | 2616 |
| CTTGTAAGTCC | | | 2617 |
| TAAACCTGTC | | | 2618 |
| CTTTCAGTTT | | | 2619 |
| TAAAAAGCAG | | | 2620 |
| CTTTGATCAG | | | 2621 |
| GTTTTGTACA | | | 2622 |
| TACCTTCCTT | | | 2623 |
| GAATGTCCTT | | | 2624 |
| GACTCTCTCA | | | 2625 |
| GACGTTCACT | | | 2626 |
| GACCTGACCC | Human zinc finger protein (ZNF154) mRNA, partial c | U20648 | 2627 |
| GACCCCCTGA | | | 2628 |
| GACCACGGCG | | | 2629 |
| CTTTTCTTTA | Human DNA/RNA-binding protein mRNA, partial cds. | U20272 | 2630 |
| GACACCGAGG | | | 2631 |
| CTTTTGTGCA | | | 2632 |

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| GAAGCATCGC | | | 2633 |
| GAAGAAAAGC | | | 2634 |
| GTTTGATTTT | Human hexokinase 1 (HK1) mRNA, complete cds. | M75126 | 2635 |
| GAAATGGGGC | | | 2636 |
| GAAAGGCACT | | | 2637 |
| CTGTGCAGAC | | | 2638 |
| GACATTGCTG | | | 2639 |
| CTAGCTCACG | | | 2640 |
| CTGTTTAAAC | Human clone 23840 mRNA, partial cds. | U79267 | 2641 |
| CTCGGATTCA | Human protein kinase mRNA, complete cds. | L33801 | 2642 |
| CTCCGGCCCA | | | 2643 |
| CTCAAGCGGC | Human tat interactive protein (TIP60) mRNA, comple | U74667 | 2644 |
| CTCAACAGAG | | | 2645 |
| TACACCAGCA | | | 2646 |
| CTAGGTAGTG | | | 2647 |
| CTGAAGAGAG | | | 2648 |
| CTACGTGCTC | | | 2649 |
| CTAAAAAATG | | | 2650 |
| CGTGGCCACG | Human mRNA for choline kinase. | D10704 | 2651 |
| CGGGCAGAAA | | | 2652 |
| CGGGAGCCGG | | | 2653 |
| TACATCCGAA | | | 2654 |
| CTATGATAGT | | | 2655 |
| CTGGATAGGA | | | 2656 |
| AAAGAAATGG | | | 2657 |
| CTGTGATTGT | Homo sapiens FLICE-like inhibitory protein long fo | U97074 | 2658 |
| CTGTCCTAGC | Human clone 23665 mRNA sequence. | U90913 | 2659 |
| TAAGATTAGA | | | 2660 |
| TAAGATTTCA | Homo sapiens heterogeneous nuclear ribonucleoprote | AF0003 | 2661 |
| CTCTCATCTC | | | 2662 |
| CTGGCCGGCT | | | 2663 |
| CTGTGTAAAG | | | 2664 |
| CTGGAAATAA | Human adrenodoxin reductase mRNA, complete cds. | J03826 | 2665 |
| CTGCTTTCTG | | | 2666 |
| CTGCTGAGCC | | | 2667 |
| CTGCCCAGTG | | | 2668 |
| CTGATGACCA | | | 2669 |
| CTGAATGCCC | | | 2670 |
| TAATAAAGAA | Human mRNA for cytokeratin 15. | X07696 | 2671 |
| GTGCCCTGTT | Homo sapiens mRNA for KIAA0587 | AB0111 | 2672 |

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| | protein, complete c | | |
| GGGCTGTTTG | | | 2673 |
| GGGGACTGGT | | | 2674 |
| CGTCCCCTCC | | | 2675 |
| GGGGCTTCTG | Human mRNA for cysteine protease, complete cds. | D55696 | 2676 |
| CGGTTCCCAC | | | 2677 |
| GGTGGATCTC | | | 2678 |
| CGGCAGGTGA | | | 2679 |
| GTAAGGTTGG | | | 2680 |
| CGGACATAGG | | | 2681 |
| CGGAACACCG | | | 2682 |
| GTCCGCCAGG | | | 2683 |
| CGGAAAAAAA | | | 2684 |
| GTGAAGCCCC | | | 2685 |
| CGACTGCACT | | | 2686 |
| CGCAAGTGGT | | | 2687 |
| CTGAACCCGG | | | 2688 |
| GTTTGCAAAC | | | 2689 |
| GTTTAAAAGA | | | 2690 |
| CGAGCATCCC | | | 2691 |
| GTGTGGGAGA | | | 2692 |
| CGCGTTAAGA | | | 2693 |
| CGCAACTTCA | | | 2694 |
| CGCCGCTTCT | | | 2695 |
| CGCAGAGGCC | | | 2696 |
| GTGGCGGACA | | | 2697 |
| CGCCGCCGGG | | | 2698 |
| GTGGAACCCC | | | 2699 |
| GTGCTGGTCA | | | 2700 |
| CGTTGGCAGG | | | 2701 |
| GTGTCTTGTA | | | 2702 |
| CTCCCCCACC | Human mRNA for KIAA0338 gene, partial cds. | AB0023 | 2703 |
| GGGCTGTTAG | | | 2704 |
| CTAGATTCGG | | | 2705 |
| CTAGGATGCG | | | 2706 |
| GCTCTGGCCG | Human mRNA for endonuclease III homolog, complete | AB0015 | 2707 |
| GCTCTCGGCG | | | 2708 |
| GCTTCCTAAA | H.sapiens mRNA for cystathionine- beta-synthase. | X82166 | 2709 |
| CTCAGATTCC | | | 2710 |
| CTACTGTCTA | | | 2711 |
| CTCTTGTGGC | | | 2712 |
| GCGGCCACCA | | | 2713 |

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| GCCTTTCCCT | | | 2714 |
| GCCTTGATGA | H.sapiens integrin associated protein mRNA, comple | Z25521 | 2715 |
| CTCTTGTGGT | | | 2716 |
| CCCTGGGAAG | | | 2717 |
| CTATTTTGT | | | 2718 |
| CTAATACTTC | | | 2719 |
| CGAAGGCTGT | NF-IL3A=interleukin-3 promoter transcriptional act | S79880 | 2720 |
| CGTTTGAAAA | | | 2721 |
| CTAAACTGG | | | 2722 |
| GGCTTGGTTT | | | 2723 |
| GGCTGCCCAG | H.sapiens mRNA for MUF1 protein. | X86018 | 2724 |
| GCTGGCAGGC | | | 2725 |
| CTAAGATTCG | | | 2726 |
| CGTGTTGAGA | | | 2727 |
| GGCCTCCCAG | Homo sapiens N-acetylglucosamyl transferase compon | AF0301 | 2728 |
| GGCACCGCGT | | | 2729 |
| GGATGTGAAA | Human MIC2 mRNA, complete cds. | M16279 | 2730 |
| CTAATGCTAG | Human mRNA for KIAA0206 gene, partial cds. | D86961 | 2731 |
| GGAGCCAGAG | | | 2732 |
| CTACCCTTTC | | | 2733 |
| GGCTCAGGGC | | | 2734 |
| CCGTAGAGGA | | | 2735 |
| CCTCCAGCCC | | | 2736 |
| TCTCTCTGCA | | | 2737 |
| CCTCAGTATA | BPTP-2=protein-tyrosine phosphatase [human, pre-B | S78086 | 2738 |
| TCTGGGGACG | | | 2739 |
| CCTATGGAAA | | | 2740 |
| TCTGTCAATC | | | 2741 |
| TCTTCCCCAG | Human selenoprotein W (seIW) mRNA, complete cds. | U67171 | 2742 |
| TCTTTCACCC | Homo sapiens mRNA for antizyme inhibitor, complete | D88674 | 2743 |
| CCTAGCCCCA | | | 2744 |
| CCTACTGCAC | | | 2745 |
| CCTACTACGT | | | 2746 |
| TGACCACCCT | | | 2747 |
| TGACTTTCCT | | | 2748 |
| GTTTGGATCT | | | 2749 |
| TGCTACGATC | | | 2750 |
| AAACGTTTCC | | | 2751 |
| TGCGAGCGCC | | | 2752 |

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| CCGAGGCAGG | | | 2753 |
| TGGAGAAAGA | | | 2754 |
| TGGAAGCATC | | | 2755 |
| CCTAAATAAA | | | 2756 |
| TGCTTGACAA | | | 2757 |
| TGAGTTGGGT | | | 2758 |
| CCGCGGTGGC | | | 2759 |
| CCGCTGGGCT | | | 2760 |
| TGCCCTGAGA | | | 2761 |
| CCGGGTGCCC | | | 2762 |
| CCGGTAATCC | | | 2763 |
| CCTCTGGGGT | | | 2764 |
| CCGCCTCCTA | | | 2765 |
| TACATTCACC | Human mRNA for protein D123, complete cds. | D14878 | 2766 |
| CCTCCAGGGT | | | 2767 |
| TAGGACCCTG | Homo sapiens mRNA for lysosomal hyaluronidase. | AJ0000 | 2768 |
| CCTGTCCACA | | | 2769 |
| CCTGTGGTTC | | | 2770 |
| TAGACTTCCT | | | 2771 |
| CCTGTCACGA | | | 2772 |
| TACCAGGAAC | | | 2773 |
| TATCCTAGGG | | | 2774 |
| CCTTGCTGTG | | | 2775 |
| TAATTTAAAA | | | 2776 |
| TAATACCAAG | | | 2777 |
| CCTTGGGTTC | | | 2778 |
| CCTTTCCTAC | | | 2779 |
| CCTTTTACCT | | | 2780 |
| CCTTCATCCT | | | 2781 |
| CCTGGCTCCC | | | 2782 |
| GCCGCCGCCG | | | 2783 |
| CCTGCATCCC | | | 2784 |
| CCTGGATCTC | | | 2785 |
| TCCAGAATAA | | | 2786 |
| CCTGGCCAGT | Human destrin-2 pseudogene mRNA, complete cds. | U72518 | 2787 |
| TAGGCCACCA | | | 2788 |
| CCTGGCCCTG | | | 2789 |
| TCTATAGCTT | | | 2790 |
| TCATCATATT | | | 2791 |
| TCAGTGACCA | Human erythroid isoform protein 4.1 mRNA, complete | J03796 | 2792 |
| CCTGGCTCGA | | | 2793 |
| CCTGGGTCAG | | | 2794 |

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| TATTAATAG | | | 2795 |
| CCTGTAATGC | | | 2796 |
| TCCAACACTACA | Homo sapiens hydroxysteroid sulfotransferase SULT2 | U92315 | 2797 |
| CACGATTAAA | | | 2798 |
| GAAGTCATT | | | 2799 |
| ATGGCCAGAA | | | 2800 |
| GAAGTAGGAC | | | 2801 |
| ATGTATGGGG | | | 2802 |
| ATGTGTTTCA | | | 2803 |
| GAAGCCATCC | | | 2804 |
| ATTGTAGACA | | | 2805 |
| ATTGTGCCAC | | | 2806 |
| ATTTGAGAAA | | | 2807 |
| GAAGACAGTG | Homo sapiens clone rasi-3 matrix metalloproteinase | U38320 | 2808 |
| GAAGAACAGA | | | 2809 |
| GGGGGACCTC | | | 2810 |
| CAAGGTCATT | Human tight junction (zonula occludens) protein ZO | L14837 | 2811 |
| GAAAAAATAA | Human dihydroorotate dehydrogenase mRNA, 3' end. | M94065 | 2812 |
| GAACCCCAGG | | | 2813 |
| GCCTGCCCTG | | | 2814 |
| GAAATCAGTG | | | 2815 |
| GAAATGTCTG | | | 2816 |
| CAGTTTGTAC | Human pyruvate dehydrogenase E1-alpha subunit mRNA | J03503 | 2817 |
| CAGTTCTCTG | | | 2818 |
| CAATTGTAAA | Homo sapiens thioredoxin-related protein mRNA, com | AF0526 | 2819 |
| CAGGTTGTGA | Human mRNA for lysosomal acid phosphatase (EC 3.1. | X12548 | 2820 |
| CACCACAACA | H. sapiens RNA for CLCN3. | X78520 | 2821 |
| CAGATTTGCA | | | 2822 |
| GAACGACCTC | | | 2823 |
| GAACGCTGAA | | | 2824 |
| GAAGTCCATA | | | 2825 |
| GAAGTGGAGA | | | 2826 |
| ATGCCCCGTGA | | | 2827 |
| GAACACCGTC | | | 2828 |
| AGACTAACAC | Human mRNA for TESK1, complete cds. | D50863 | 2829 |
| ATGGCAAGGT | | | 2830 |
| GACGAGCCAC | Homo sapiens mRNA from chromosome 5q21-22, clone:F | AB0024 | 2831 |

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| AGGACTTCTG | | | 2832 |
| GACGCGGCGC | | | 2833 |
| AGCCTGCCTG | Human heat shock factor 1 (TCF5) mRNA, complete cd | M64673 | 2834 |
| AGGGCCCTCA | | | 2835 |
| AGAGCAAACC | Homo sapiens lysyl hydroxylase (PLOD) mRNA, comple | L06419 | 2836 |
| AGGGGGGAGG | | | 2837 |
| AGAACCTTTG | | | 2838 |
| GACGTGATGG | Homo sapiens KIAA0406 mRNA, complete cds. | AB0078 | 2839 |
| ACTTTTTCAC | | | 2840 |
| ACTGTGGTTT | | | 2841 |
| ACTGTCTGTC | | | 2842 |
| ACTGTAATCC | | | 2843 |
| GACGGCTACT | | | 2844 |
| GAATTCCTCG | | | 2845 |
| CCCAACCCCT | Human DRPLA mRNA for ORF, complete cds. | D31840 | 2846 |
| ATGCAGAGAT | | | 2847 |
| GAAGTTTTTT | | | 2848 |
| GAATCGAAGT | | | 2849 |
| GAATCTCAGC | | | 2850 |
| GACCCTTCTC | | | 2851 |
| GAATGATTTC | | | 2852 |
| ATGCTAGATT | | | 2853 |
| ATCAAATGCA | Human (Daudi) translocated t(8;14) c-myc oncogene | K02276 | 2854 |
| ATAGATGGGG | | | 2855 |
| GACAGCCATC | | | 2856 |
| GACCCAGGAG | | | 2857 |
| AGTAGCGAAC | H.sapiens HCG V mRNA. | X81003 | 2858 |
| AGGTACTGGT | H.sapiens c-abl mRNA 3'-fragment. | X51945 | 2859 |
| GAATCTTCTC | | | 2860 |
| GAGTTCCTCG | Homo sapiens erythroid K:Cl cotransporter splicing | AF0545 | 2861 |
| GAATAAATGT | | | 2862 |
| CTGTCCGGCT | | | 2863 |
| CTGGTCCTGG | | | 2864 |
| CTGGGCTACT | | | 2865 |
| CTGGGATCTG | | | 2866 |
| CTGGCCTGTA | | | 2867 |
| CTGGCACTTA | | | 2868 |
| CTGGAGCCGC | | | 2869 |
| GAGCTGTTGG | Homo sapiens integrin alpha E mRNA, complete cds. | L25851 | 2870 |

| | | | |
|------------|--|--------|------|
| CTGCTTTTTT | Homo sapiens clone 24658 mRNA sequence. | AF0550 | 2871 |
| GAGGCATATG | | | 2872 |
| GAGGCTCCGA | | | 2873 |
| GAGGGGAGGA | | | 2874 |
| GAAAGTGCAG | Homo sapiens mRNA for VRK2, complete cds. | AB0004 | 2875 |
| CTGCCCTCCC | Human alpha-L-iduronidas (IDUA) mRNA, complete cds | M74715 | 2876 |
| CTGATGTTCC | | | 2877 |
| CTGATTTATT | | | 2878 |
| GCAGCCTGGA | | | 2879 |
| CTGCAAAGGA | Homo sapiens phospholipase D2 (PLD2) mRNA, splice | AF0384 | 2880 |
| GCACCTTCTG | | | 2881 |
| CTGCTGGGCA | | | 2882 |
| CTGCAGAATA | | | 2883 |
| GAGTTATGAG | | | 2884 |
| GATTGGACTT | | | 2885 |
| CTGCGAGTGA | | | 2886 |
| CTGCTGAAGT | | | 2887 |
| GATCAAGGGT | | | 2888 |
| CTGCTGCCCC | | | 2889 |
| CTGTGCTCTA | | | 2890 |
| GCACAAGAGT | | | 2891 |
| CCTCCCTGCT | | | 2892 |
| CTGTGCTCAC | | | 2893 |
| CCTTGTTTTT | Homo sapiens UEV-1 (UBE2V) alternatively spliced i | U97279 | 2894 |
| CTTCCCTCA | | | 2895 |
| CCTGTAATTC | Homo sapiens mRNA for KIAA0591 protein, partial cd | AB0111 | 2896 |
| CTTTCCTTTT | Human uncoupling protein homolog (UCPH) mRNA, comp | U94592 | 2897 |
| CTTGTGAGGC | | | 2898 |
| CTTTTAAAAT | Homo sapiens mRNA for cytochrome c, partial cds. | D00265 | 2899 |
| CTTGCCTGAA | Homo sapiens amphiphysin II mRNA, complete cds. | AF0013 | 2900 |
| CCTATCATAT | | | 2901 |
| CCCGTCCCGG | | | 2902 |
| CCCCTGCCAT | | | 2903 |
| CCCCACCGCC | Homo sapiens DCHT mRNA, complete cds. | AF0176 | 2904 |
| CTTTTGGCTG | Human squalene synthetase (ERG9) mRNA, complete cd | L06070 | 2905 |

| | | | |
|-------------|--|--------|------|
| CCCATCCGCA | | | 2906 |
| CTTTCTGGGC | Human putative outer mitochondrial membrane 34 kDa | U58970 | 2907 |
| CTTCATAAGG | | | 2908 |
| TGGTTGAACC | Homo sapiens TTAGGG repeat binding factor 2 (hTRF2 | AF0029 | 2909 |
| CTTTTCAAGA | H.sapiens, gene for Membrane cofactor protein. | X59408 | 2910 |
| CTGTTAATCA | | | 2911 |
| CTGTTTGTG | | | 2912 |
| CTTCAACAAC | | | 2913 |
| CTTTAGCTAC | | | 2914 |
| CTGGATGGGC | | | 2915 |
| GAAGGTGGAG | | | 2916 |
| CTGCCCTGGG | | | 2917 |
| CTTCTAGCAA | | | 2918 |
| CTTCTTTCCA | | | 2919 |
| CTCTGTTGAT | Human antioxidant enzyme AOE37-2 mRNA, complete cd | U25182 | 2920 |
| CTACCAGGAA | | | 2921 |
| CTAACGCAGC | | | 2922 |
| CTTCAGGCAA | | | 2923 |
| AGAATAAAAT | | | 2924 |
| AGCTTCCGCT | | | 2925 |
| AGCTGGATGC | | | 2926 |
| AGCCTCCCAG | | | 2927 |
| AGCCCTGGAC | | | 2928 |
| AGCCCAGGAG | | | 2929 |
| AGCCCAGCTG | | | 2930 |
| AGCCAACTCA | | | 2931 |
| AGCAGCCCCT | | | 2932 |
| AGATGGACAT | | | 2933 |
| AGATCCTACT | squalene synthase=farnesyl diphosphate:farnesyl di | S76822 | 2934 |
| AGAGCCCAAG | | | 2935 |
| AGAGATCACA | | | 2936 |
| AGACTTGTTT | | | 2937 |
| ACGTGACACC | Homo sapiens mRNA for KIAA0541 protein, partial cd | AB0111 | 2938 |
| ACTCCTGCCT | | | 2939 |
| ATATTTTCATT | Homo sapiens mRNA variant beta for RNA polymerase | AJ2241 | 2940 |
| ACTACCCCTG | | | 2941 |
| ACTAGAAACC | | | 2942 |
| ACTCAAATCT | | | 2943 |
| ACTCAGGTGA | | | 2944 |

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|------------|--|--------|------|
| AGACAGCCGC | | | 2945 |
| ACTCCAGTGC | | | 2946 |
| AGAATAAACG | | | 2947 |
| ACTGACGCTT | | | 2948 |
| ACTTCACCCT | | | 2949 |
| ACTTCCTTCC | Human ionotropic ATP receptor P2X5b mRNA, complete | U49396 | 2950 |
| ACTTCTTCAC | | | 2951 |
| ACTTTTTAAA | | | 2952 |
| AGGAATTTGA | | | 2953 |
| ACTCCAGAAA | | | 2954 |
| AGTGATTTGC | | | 2955 |
| AGCTTTTTAA | H.sapiens small nucleolar RNA U36a. | X97584 | 2956 |
| AGTCCTTATG | | | 2957 |
| AGTCTCTGTT | | | 2958 |
| AGTGAACCCA | | | 2959 |
| AGTGACCGAA | | | 2960 |
| AGTATCCTCC | | | 2961 |
| AGTGATGGCG | | | 2962 |
| AGTATCAATC | | | 2963 |
| AGTGTACTCC | | | 2964 |
| AGTTTCAGAG | | | 2965 |
| ATAAAGAAGG | | | 2966 |
| ATAATTTTTA | | | 2967 |
| ATACATAATT | | | 2968 |
| CCCTTCTGGC | | | 2969 |
| AGTGAGGATG | | | 2970 |
| AGGCTGGACG | | | 2971 |
| ACGGCCGCCT | | | 2972 |
| AGGACAAACC | Homo sapiens GDP-mannose 4,6 dehydratase mRNA, com | AF0423 | 2973 |
| AGGACAAGTC | | | 2974 |
| AGGACGTCAT | | | 2975 |
| AGGAGCCTCA | Human collagen type XII alpha-1 precursor (COL12A1 | U73778 | 2976 |
| AGTCAAGCCC | Homo sapiens skeletal muscle LIM-protein FHL3 mRNA | U60116 | 2977 |
| AGGCTCTGAG | | | 2978 |
| AGGAAGCTGA | Human mRNA for uracil-DNA glycosylase. | X52486 | 2979 |
| AGGGCACTGA | | | 2980 |
| AGGGCAGGGA | Homo sapiens RaP2 interacting protein 8 (RPIP8) mR | U93871 | 2981 |
| AGGGCCGACT | H.sapiens mki67a mRNA (short type) for antigen of | X65551 | 2982 |
| AGGGCTGCCA | | | 2983 |

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|------------|--|--------|------|
| AGGGCTTTCC | | | 2984 |
| AGGGTTGCTT | | | 2985 |
| AGGAGCCTTA | | | 2986 |
| AAGCTCCATC | | | 2987 |
| AATGTCCAGT | | | 2988 |
| AATGTCAGCA | | | 2989 |
| AATGGGGGTT | | | 2990 |
| AATGGGGAGA | | | 2991 |
| AATATTAAGA | Homo sapiens U5 snRNP 100 kD protein mRNA, complet | AF0264 | 2992 |
| AATATCTTGC | | | 2993 |
| AATATCTGAC | Human guanine nucleotide regulatory protein (ABR) | U01147 | 2994 |
| AATATCATTG | | | 2995 |
| AATACACAGA | | | 2996 |
| AATAAAAGTG | H.sapiens mRNA for phospholipase C-b3. | Z26649 | 2997 |
| AAGTTTTCTT | | | 2998 |
| AAGTATGTGA | | | 2999 |
| AAGGTGCTGG | | | 3000 |
| ACGTGAGTGC | | | 3001 |
| AACGGACTCT | | | 3002 |
| AAAGGATAAT | Human basic transcription factor BTF2p44 mRNA, 3' | U21910 | 3003 |
| AAAGGCACTG | | | 3004 |
| AACACAGTGC | | | 3005 |
| AACCAATCTG | | | 3006 |
| AACCATTTTT | | | 3007 |
| AAGGAAGATA | | | 3008 |
| AACCCAATCC | | | 3009 |
| AAGGAAAACG | | | 3010 |
| AACTTTTGGC | | | 3011 |
| AAGAACTTTG | | | 3012 |
| AAGAAGGCAA | Human albumin D-box binding protein mRNA, complete | U79283 | 3013 |
| AAGAGCGACT | | | 3014 |
| AAGAGCTTGC | | | 3015 |
| AATTCCCGTC | | | 3016 |
| AACCCAAAAA | Human (nmc) mRNA, partial cds. | U31214 | 3017 |
| ACCTGCATCA | Homo sapiens mRNA for protein phosphatase 2C gamma | Y13936 | 3018 |
| AATGTGTCTC | | | 3019 |
| ACCCGCGTGC | Human chorionic gonadotropin (hcg) beta subunit mR | J00117 | 3020 |
| ACCCTGGCCC | | | 3021 |
| ACCCTGGCTG | | | 3022 |

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|-------------|---|--------|------|
| ACCGCCGGGC | | | 3023 |
| ACCATCTCTG | | | 3024 |
| ACCTCCGTGT | Human angiotensinogen mRNA, complete CDS. | K02215 | 3025 |
| ACCAGGTGGA | | | 3026 |
| ACCTGGCTTT | | | 3027 |
| ACCTGTTGCC | | | 3028 |
| ACCTTGACAC | | | 3029 |
| ACCTTGTAAT | | | 3030 |
| ACGAGGATCT | | | 3031 |
| ACGATGCTGC | | | 3032 |
| ACCTCCATTT | Human c-sis oncogene mRNA, 3' flank. | M32009 | 3033 |
| ACACTTCTTG | | | 3034 |
| ATCAAGTTCC | | | 3035 |
| ACAAAATAAA | Homo sapiens NRF1 protein (NRF1) mRNA. | L24123 | 3036 |
| ACAAACCCCC | | | 3037 |
| ACAAGCATCC | | | 3038 |
| ACACAGACGG | | | 3039 |
| ACCCACTTTC | Human mRNA for KIAA0310 gene, complete cds. | AB0023 | 3040 |
| ACACAGGCTT | | | 3041 |
| AATTATGCGG | | | 3042 |
| ACACTTCTTT | Human G protein gamma-11 subunit mRNA, complete cd | U31384 | 3043 |
| ACACTTTTTT | | | 3044 |
| ACAGCTTTGT | | | 3045 |
| ACATAAGACA | | | 3046 |
| ACATCTGGCT | | | 3047 |
| ACATTGGGTA | | | 3048 |
| ACACAGCTCT | | | 3049 |
| CCAACCTCCTA | | | 3050 |
| CCCATCGTCG | | | 3051 |
| CCCACTCTTT | | | 3052 |
| CCCACTATGT | | | 3053 |
| CCCAAGAGAA | | | 3054 |
| CCCAACGCTG | | | 3055 |
| CCCAAAGCAC | | | 3056 |
| CCATCCAGTG | | | 3057 |
| CCAGTCTGGG | | | 3058 |
| CCAGGGCTGA | | | 3059 |
| CCAGGAGGAG | | | 3060 |
| CCAGCAGTGG | | | 3061 |
| CCACTGGCAC | | | 3062 |
| CCACAGTAGA | Homo sapiens zinc finger transcription factor (ZNF | AF0460 | 3063 |

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|------------|--|--------|------|
| CAGGCCTTGG | | | 3064 |
| CATCTTTTAA | Homo sapiens dolichol monophosphate mannose syntha | AF0078 | 3065 |
| ATATGCCACA | | | 3066 |
| CAGGTGACAA | Human mRNA for KIAA0304 gene, complete cds. | AB0023 | 3067 |
| CAGGTGCTGG | | | 3068 |
| CAGTATTTAA | | | 3069 |
| CAGTGGTCTG | Human replication factor C large subunit mRNA, com | L23320 | 3070 |
| CCACAGGCAG | | | 3071 |
| CATATGAAAA | | | 3072 |
| CCAAGGGTCC | | | 3073 |
| CATTCATTGG | | | 3074 |
| CATTGTAAAT | Human maspin mRNA, complete cds. | U04313 | 3075 |
| CATTGTCTTC | | | 3076 |
| CATTTGGGAA | | | 3077 |
| CCAAACCATC | | | 3078 |
| CCCCAGGAGA | | | 3079 |
| CATAACTTAC | | | 3080 |
| TTAGTTACCT | | | 3081 |
| CCCATTGCA | | | 3082 |
| TTGCCATTGG | | | 3083 |
| TTCTGGTGCG | | | 3084 |
| TTCTGCCCCC | H.sapiens mRNA 3'-region (unknown function). | Y12338 | 3085 |
| TTCTCTACAA | | | 3086 |
| CCCTCCCAGG | | | 3087 |
| TTATCGTCCT | | | 3088 |
| TTGTCCGGGC | Human tubulin-folding cofactor C mRNA, complete cd | U61234 | 3089 |
| TTACTATTCA | Homo sapiens mRNA for putative glucosyltransferase | AJ2248 | 3090 |
| CCCTCGAAGC | | | 3091 |
| TTAAGTGGAA | | | 3092 |
| CCCTGAATCC | | | 3093 |
| TGTGAGCCCT | | | 3094 |
| CCCTGCCCCC | | | 3095 |
| TTCCCTGGGA | | | 3096 |
| CCCCTCCCCT | | | 3097 |
| CAGGCCAACC | | | 3098 |
| CCCCCACC | | | 3099 |
| CCCCCTTGCA | Human mRNA for GC-Box binding protein BTEB2, compl | D14520 | 3100 |
| CCCCGCAGCT | | | 3101 |
| CCCCTACATC | | | 3102 |

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|-------------|---|--------|------|
| CCCTCCTGGA | | | 3103 |
| TTTGT CAGGC | | | 3104 |
| CCCCAGCTGC | | | 3105 |
| CCCCTCCTGG | | | 3106 |
| CCCCTTCCGG | | | 3107 |
| CCCGAGGCAG | | | 3108 |
| TTTATTCCTC | | | 3109 |
| CCCGGCCAGC | | | 3110 |
| TTGTTGCTGA | | | 3111 |
| CCCCTCCAGC | | | 3112 |
| ATGCTTCAGG | | | 3113 |
| ATTACACTAC | | | 3114 |
| ATGTTGAGAT | | | 3115 |
| ATGTCTTTTA | | | 3116 |
| ATGTCTTAAT | | | 3117 |
| ATGTCCCCTG | | | 3118 |
| ATGTATTCTT | | | 3119 |
| ATGTACAGGT | | | 3120 |
| ATGGGTTTGC | | | 3121 |
| ATGGGGGTGA | | | 3122 |
| ATGGGATTCT | | | 3123 |
| ATGGCTAGTA | | | 3124 |
| ATGGCACTTT | | | 3125 |
| ATGGCAATTT | | | 3126 |
| CAGGCTTCAC | Human mRNA for KIAA0247 gene, complete cds. | D87434 | 3127 |
| ATGAGATGAG | | | 3128 |
| ATCATTCCCT | | | 3129 |
| ATCCGCCGAA | | | 3130 |
| ATCCGCTGCG | | | 3131 |
| ATCTATTGAA | | | 3132 |
| ATCTGGGGCC | | | 3133 |
| ATGGCAAAGA | | | 3134 |
| ATGAAAAAAA | | | 3135 |
| ATGCTTTGAA | | | 3136 |
| ATGAGATGCT | Human neuroendocrine-dlg (NE-dlg) mRNA, complete c | U49089 | 3137 |
| ATGAGCAACT | Human MAP kinase phosphatase (MKP-2) mRNA, complet | U48807 | 3138 |
| ATGATGTCCT | | | 3139 |
| ATGCACATAA | H.sapiens mRNA for apolipoprotein E receptor 2. | Z75190 | 3140 |
| ATGCAGAATT | | | 3141 |
| ATTCTTTCCT | | | 3142 |
| ATCTTCGCTT | Human mRNA for KIAA0067 gene, complete cds. | D31891 | 3143 |

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|-------------|--|--------|------|
| CAGCAGCTGC | Human HepG2 partial cDNA, clone hmd3b11m5. | D17022 | 3144 |
| ATTAGTCAGA | Human testicular inhibin beta-B-subunit mRNA, 3' e | M31682 | 3145 |
| CACGCTCACT | | | 3146 |
| CACTATGCAC | | | 3147 |
| CACTATTCAC | | | 3148 |
| CAGACTCCCG | | | 3149 |
| CACCAAATA | | | 3150 |
| CAGCACGAAA | | | 3151 |
| CACCAAAAAA | | | 3152 |
| CAGCCGAGGC | | | 3153 |
| CAGCTATCAT | | | 3154 |
| CAGCTGCAGA | | | 3155 |
| CAGCTTAATT | | | 3156 |
| CAGGAAAGGC | | | 3157 |
| CAGGACGGGC | H.sapiens encoding CLA-1 mRNA. | Z22555 | 3158 |
| CAGCACCAGG | Human 5'-AMP-activated protein kinase, gamma-1 sub | U42412 | 3159 |
| ATTTTTTCCA | | | 3160 |
| GACTCGTGGA | | | 3161 |
| ATTGCGCCAC | | | 3162 |
| ATTTACAAGA | | | 3163 |
| ATTTCTGTTGG | | | 3164 |
| ATTTCTCTAA | | | 3165 |
| CACCCTAATT | | | 3166 |
| ATTTTAAGGG | | | 3167 |
| ATTATGGGCA | Human nuclear factor kappa-B DNA binding subunit (| M58603 | 3168 |
| CAAAATTCAG | | | 3169 |
| CAACTCTATG | Human DNA topoisomerase II (top2) mRNA, complete c | J04088 | 3170 |
| CAAGAAGAGC | | | 3171 |
| CAAGCGCTCT | Homo sapiens clone cRT16 CREB-binding protein mRNA | U89355 | 3172 |
| CAAGGGGGCA | | | 3173 |
| CACAATATTG | | | 3174 |
| ATTTGTGAGC | | | 3175 |

Table 2

Breast Cancer - Transcripts downregulated in metastatic breast tumor cells

| Accession | Description | Accession | Size (nt) |
|------------|--|-----------|-----------|
| GTGCGGAGGA | Human mRNA for serum amyloid A (SAA) protein parti | X51441 | 3176 |
| TACCTGCAGA | Human mRNA for cystic fibrosis antigen (CFAg). | Y00278 | 3177 |
| CTCGGGGGAA | Homo sapiens serum amyloid A2-beta (SAA2) mRNA, co | M23700 | 3178 |
| GGTCAGTCGG | | | 3179 |
| GTTACATTA | Human mRNA for HLA-DR antigens associated invarian | X00497 | 3180 |
| GCCCAGCATT | Homo sapiens prostate stem cell antigen (PSCA) mRN | AF0434 | 3181 |
| ACCCGCCGGG | | | 3182 |
| AGAGGTGTAG | | | 3183 |
| GTGGCCACGG | Human mRNA for calcium-binding protein in macropha | X06233 | 3184 |
| GTGACCACGG | | | 3185 |
| TGGCCCTCAG | | | 3186 |
| GACTCTTCAG | Human alpha-1-antichymotrypsin mRNA, 3' end. | J05176 | 3187 |
| CCGACGGGCG | | | 3188 |
| CCGGCCCTAC | Human DD96 mRNA, complete cds. | U21049 | 3189 |
| TACCTCTGAT | H.sapiens mRNA for calcium-binding protein S100P. | X65614 | 3190 |
| CCTGAGGGTA | | | 3191 |
| ATTGGCTTAA | prohibitin [human, mRNA, 1043 nt]. | S85655 | 3192 |
| GCCTTAACAA | Human pre-B cell enhancing factor (PBEF) mRNA, com | U02020 | 3193 |
| ATGGTGCACG | | | 3194 |
| ACCAGCATAG | | | 3195 |
| CTGCAGGGCC | | | 3196 |
| CTAACTAGTT | | | 3197 |
| GGTTTGGCTT | Human mRNA for mitochondrial hinge protein. | Y00764 | 3198 |
| ATCCTTGCTG | Human radiated keratinocyte mRNA for cysteine prot | X05978 | 3199 |
| TCTCAATTCT | | | 3200 |
| TGCCCTCAGG | | | 3201 |
| TTGAATCCCC | H.sapiens encoding skin-derived antileukoproteinas | Z18538 | 3202 |
| TGGAAGCACT | Human monocyte-derived neutrophil-activating prote | M26383 | 3203 |
| GCAGGAGGTG | | | 3204 |

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|------------|--|--------|------|
| GTGGGCCACG | | | 3205 |
| GCCGTTCTTA | | | 3206 |
| GTGGCCCACG | | | 3207 |
| GAGCAGCGCC | psoriasin {3' region} [human, psoriatic skin lesio | S81991 | 3208 |
| CTAATAAACT | | | 3209 |
| CGAGCTTCCA | | | 3210 |
| CAGACTTTTT | | | 3211 |
| GCACAGAGCT | | | 3212 |
| GATCTCGCAA | | | 3213 |
| TCCTGCAGCT | | | 3214 |
| GGCTGGGGGG | | | 3215 |
| CCTGCTGCAG | | | 3216 |
| TGGCCCTCAA | | | 3217 |
| CAAGTTTGCT | | | 3218 |
| CAAGGGCTTG | | | 3219 |
| ATTTTCTAAA | | | 3220 |
| TGAGGAAGAC | Human ionizing radiation resistance conferring pro | U18321 | 3221 |
| CTGAGAAACT | | | 3222 |
| GAGGCTCAAT | | | 3223 |
| CACCTAAATT | | | 3224 |
| ATCCATCTGT | H.sapiens hnRNP-E2 mRNA. | X78136 | 3225 |
| TGGCGTACGG | | | 3226 |
| TTGTAAACTT | Human FK506-binding protein 25 (FKBP25) mRNA, comp | M90309 | 3227 |
| TTGGGGGTTC | | | 3228 |
| AAGATAATGC | | | 3229 |
| GGCAACGTGG | | | 3230 |
| GATTGGGGAT | | | 3231 |
| TGTGTTGAAG | | | 3232 |
| AATAAATGGA | | | 3233 |
| GGGCCTGACA | | | 3234 |
| TGCCCTCCAG | | | 3235 |
| ATTAAGAGGG | | | 3236 |
| CCCCAGCCCC | | | 3237 |
| CCCATCGGCC | | | 3238 |
| ACCGCCGTGG | Human neutrophil cytochrome b light chain p22 phag | M21186 | 3239 |
| AAGGTGGCAA | | | 3240 |
| GACCAGCTGC | | | 3241 |
| CTGATGGCGA | | | 3242 |
| AATGGATGAA | | | 3243 |
| CCTATGTAAG | H.sapiens mRNA gene for hnRNP G protein. | Z23064 | 3244 |
| CCTGGATAAA | | | 3245 |

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|------------|--|--------|------|
| AGAAGATCTG | | | 3246 |
| ACCCAGAGCT | | | 3247 |
| TGTCTGATGC | | | 3248 |
| TAATTTTGAA | | | 3249 |
| TTCCCTCGTG | | | 3250 |
| GCAACAACAC | | | 3251 |
| AATGCAAAAT | | | 3252 |
| AACGCAGGAG | | | 3253 |
| CTAAGAACTT | | | 3254 |
| GTGGCCAAGG | | | 3255 |
| CCCTTGAGGA | Human small proline rich protein (sprl) mRNA, clon | M19888 | 3256 |
| TTTACTGGTA | | | 3257 |
| AGCAGAGATC | | | 3258 |
| TTGAAACTTT | Human gro (growth regulated) gene. | J03561 | 3259 |
| CCCGCTCTTG | | | 3260 |
| AGGGAGGCAG | | | 3261 |
| CCCAGGCCCA | | | 3262 |
| GTGCCGACAG | | | 3263 |
| CACCAATGTG | | | 3264 |
| CCAAAAAAA | Human interferon-induced leucine zipper protein (l | U72882 | 3265 |
| GGATCCTCGG | | | 3266 |
| TTATGCTTTC | | | 3267 |
| CCTGTGTTGG | | | 3268 |
| AAATTGTTCC | Human mRNA for proteasome subunit HC8. | D00762 | 3269 |
| CCTAGCTGGG | | | 3270 |
| GGCAGCAATG | Human mRNA fragment for mesothelial type II kerati | X03212 | 3271 |
| AGGTCCACCA | | | 3272 |
| ACACTACGGG | | | 3273 |
| CTGGCCCTCG | Human estrogen receptor mRNA, partial cds. | M12075 | 3274 |
| AATATATCCA | | | 3275 |
| CTCGCGCTGG | | | 3276 |
| CTTAATCCTG | | | 3277 |
| CCACAAACGG | | | 3278 |
| TGCCCTCAA | | | 3279 |
| GGCTTGCCAG | | | 3280 |
| TGCCCTCAGA | | | 3281 |
| TTTGAAATGA | Spermidine/spermine N1-acetyltransferase mRNA, com | M77693 | 3282 |
| AGCTCTTGGA | | | 3283 |
| TACCTGGCAG | Homo sapiens clone 23579 mRNA sequence. | AF0381 | 3284 |

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|------------|--|--------|------|
| GACTAACACC | | | 3285 |
| GATTCCTTG | H.sapiens ADE2H1 mRNA showing homologies to SAICAR | X53793 | 3286 |
| GCAATAAATG | Human mRNA for drebrin E, complete cds. | D17530 | 3287 |
| GCCCGTCCGG | | | 3288 |
| ACCCACCTGC | | | 3289 |
| TGGTTTTGGC | | | 3290 |
| GACCCCTGTC | Homo sapiens (clone s153) mRNA fragment. | L40391 | 3291 |
| CCGAGGCTGC | | | 3292 |
| TACCTGCCAG | | | 3293 |
| TGAAGAGAAG | Human mRNA for KIAA0106 gene, complete cds. | D14662 | 3294 |
| GAGTTGGGTA | | | 3295 |
| GATTGATGTC | Human 38 kDa Mov34 isologue mRNA, complete cds. | U70734 | 3296 |
| TACAGGAAGT | | | 3297 |
| GGGCTGGGGG | | | 3298 |
| GAGTGAGCAG | | | 3299 |
| TAATTTGCGT | | | 3300 |
| GTGGTATGTG | | | 3301 |
| GGGGACGGGA | | | 3302 |
| GGTGGCTTTG | Homo sapiens NADH-ubiquinone oxidoreductase subuni | AF0471 | 3303 |
| GTGGCTCTAT | | | 3304 |
| GTGATGGCCA | | | 3305 |
| TAACAGTTGT | | | 3306 |
| AGGAGAGGGA | | | 3307 |
| TGCAGATATT | Human protein phosphatase (KAP1) mRNA, complete cd | L27711 | 3308 |
| TGCCCCTCAG | | | 3309 |
| GCTAAACTGC | | | 3310 |
| TTTTTCTTAA | | | 3311 |
| ACAGCCTGCA | | | 3312 |
| TGGTGTATGC | | | 3313 |
| TACTGGTTTA | | | 3314 |
| TTTATTTAGC | Homo sapiens clone 24707 mRNA sequence. | AF0550 | 3315 |
| ACGCAGGGAG | | | 3316 |
| TTGGGTCCTC | | | 3317 |
| AGCAACAGTG | Human endothelial-monocyte activating polypeptide | U10117 | 3318 |
| ACCAGGCAAG | | | 3319 |
| AGCTTATTGA | | | 3320 |
| GAGCCAGGTG | Human retinoic acid-responsive | U50383 | 3321 |

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| | protein (NN8-4AG) m | | |
| TTGGGGTTCA | | | 3322 |
| ATGAAACCCT | | | 3323 |
| CAGAGGCCCT | H.sapiens IKBL mRNA. | X77909 | 3324 |
| TTCTCTCCAA | | | 3325 |
| CCCAGAACAG | | | 3326 |
| CCCTAATTGG | | | 3327 |
| CCTGAGTTGA | | | 3328 |
| GAGAACCGTA | | | 3329 |
| CTCACTTCTT | | | 3330 |
| CTGGTTGTAG | | | 3331 |
| GACCCTAGCT | | | 3332 |
| GTGTCTCATC | H.sapiens mRNA for 2-phosphopyruvate-hydratase-alp | X84907 | 3333 |
| GGGTGCAAAA | | | 3334 |
| TAAGGTTGTC | | | 3335 |
| TAAGCAGATG | | | 3336 |
| AGGTCCTGCT | | | 3337 |
| AGTCTGTCCA | Human mRNA for prolyl 4-hydroxylase beta subunit (E | X05130 | 3338 |
| TGCAGGCCTG | H.sapiens mRNA for IFP53. | X62570 | 3339 |
| GTGGGTTGGC | Human aldehyde dehydrogenase 2 mRNA. | K03001 | 3340 |
| GGATGTAGAG | | | 3341 |
| CAGCGCCACC | Homo sapiens serine threonine kinase 11 (STK11) mR | AF0356 | 3342 |
| CATTCAGTTG | | | 3343 |
| GTGCTAGATT | | | 3344 |
| ATGAGCTGAC | Homo sapiens cystatin B mRNA, complete cds. | L03558 | 3345 |
| CCCCCGTACA | | | 3346 |
| ACCACAGTTT | | | 3347 |
| GGTGGCACTG | | | 3348 |
| GCGGCGACTA | | | 3349 |
| GGGGCAGGCC | | | 3350 |
| GTTGTCTTTG | Human complement component C3 mRNA, alpha and beta | K02765 | 3351 |
| CGTCTGTAAG | | | 3352 |
| CTATGGTGTT | HNL=neutrophil lipocalin [human, ovarian cancer ce | S75256 | 3353 |
| TAGGACAAC | | | 3354 |
| GCCGAAGGAA | | | 3355 |
| GCCCTGCTGG | | | 3356 |
| GCCCGGGTGG | | | 3357 |
| GCCCCAGCAT | | | 3358 |
| GCAAAATCCC | | | 3359 |

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| GAAACTGTGA | | | 3360 |
| GAGGGTTCCA | | | 3361 |
| GACACAGCAA | | | 3362 |
| CCCCTATTAA | | | 3363 |
| TCTTGATGTC | | | 3364 |
| AAGGATGCCA | Human mRNA for GATA-3 transcription factor. | X55122 | 3365 |
| TTGCGTTGCG | | | 3366 |
| TTTCCTTCCT | Human brain-type clathrin light-chain a mRNA, comp | M20471 | 3367 |
| TGGCACGTTT | | | 3368 |
| TGCCCCTCAA | | | 3369 |
| AACAATTGGG | H.sapiens fus-chop mRNA for fusion protein. | X71427 | 3370 |
| TGCCCCCAGG | | | 3371 |
| TCCACTACCA | | | 3372 |
| TCTGTCCCCC | | | 3373 |
| TGGGTTTTAA | | | 3374 |
| TCAATAAAGG | | | 3375 |
| AAGTTTGCCT | Human mRNA for glutaredoxin, complete cds. | D21238 | 3376 |
| TTGGGTATCC | Human glutamine:fructose-6-phosphate amidotransfer | M90516 | 3377 |
| TTTCCTTTGC | | | 3378 |
| TAGGTTTCGTG | Human cysteinyl-tRNA synthetase mRNA, partial cds. | L06845 | 3379 |
| TTTAGTGACG | | | 3380 |
| TGACTAATTG | | | 3381 |
| TCGAAGAACC | Human mRNA for melanoma-associated antigen ME491. | X07982 | 3382 |
| GGAAGGGGAG | H.sapiens mRNA for NF-kB subunit. | X61498 | 3383 |
| CTGAAAAAAA | | | 3384 |
| TATGAGATAG | | | 3385 |
| TACTGCTCGG | | | 3386 |
| GCCTGGAGGG | | | 3387 |
| TTCATACACT | | | 3388 |
| CTGAGCAACA | | | 3389 |
| TTCTCTCCCC | | | 3390 |
| GTTCCAGCAG | | | 3391 |
| ATGGAACCCA | | | 3392 |
| ATGAAAGGTT | | | 3393 |
| GGAATCCAAT | | | 3394 |
| CTGATGGCCA | | | 3395 |
| AGTCAGTGGG | | | 3396 |
| GAGGAAGGCT | | | 3397 |
| AGGTGTGTCA | | | 3398 |

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| GAGCAGCTGG | Human copine I mRNA, complete cds. | U83246 | 3399 |
| GAGCAGATCA | | | 3400 |
| AGCTTCTACC | Human small proline rich protein (sprll) mRNA, clo | M21302 | 3401 |
| AGCAAAGTGA | | | 3402 |
| TTGCCAACAC | H.sapiens mRNA for a novel synaptophysin related p | X61382 | 3403 |
| CGTCCTACGT | | | 3404 |
| AGTGTCCGGC | | | 3405 |
| CCCAAGTGCC | | | 3406 |
| CCAATGGACA | | | 3407 |
| GCTTTGTATC | E2k=alpha-ketoglutarate dehydrogenase complex dihy | S72422 | 3408 |
| GAAACTGAAG | | | 3409 |
| CCACTGAACT | | | 3410 |
| GTGAAAGGCA | | | 3411 |
| CCAGTACAGC | | | 3412 |
| GCGGCGGCTC | | | 3413 |
| CCCCCAGCCA | | | 3414 |
| CCCCTGGGTT | | | 3415 |
| AGGTGGCAAA | | | 3416 |
| TTGTAAACAT | Human nucleolar protein p40 mRNA, complete cds. | U86602 | 3417 |
| GCGTGCTCAC | | | 3418 |
| GCTCACGTCG | | | 3419 |
| CCGTAGTGCC | | | 3420 |
| CCCGTTCCGG | | | 3421 |
| CTGTGTCTGT | | | 3422 |
| ACACTTGGAG | | | 3423 |
| GTATTTAACT | | | 3424 |
| TCCCCGTACT | | | 3425 |
| CAATGTGAGC | | | 3426 |
| CTAAGGTGGG | Human mRNA for protein phosphatase 2A 74 kDa regul | D78360 | 3427 |
| CAATTTAAGT | H.sapiens HCGVII mRNA. | X80916 | 3428 |
| CAGTGTTGCG | | | 3429 |
| GCCTGTAATC | | | 3430 |
| GTGAAATCCC | Human sno oncogene mRNA for snoA protein, ski-rela | X15217 | 3431 |
| CCAAATGCTG | | | 3432 |
| GCTGGGGACT | H.sapiens mRNA for monoamine-sulfating phenosulfot | X84653 | 3433 |
| GCCTGTAATG | | | 3434 |
| CACGTTCCCT | Human mRNA for KIAA0263 gene, complete cds. | D87452 | 3435 |
| AAGGTTTCTG | | | 3436 |

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| CAGGACAGTT | | | 3437 |
| TGAAGTAACA | | | 3438 |
| GAGTTATGTT | | | 3439 |
| ATGGTGGTGG | Homo sapiens secretory carrier membrane protein (S) | AF0050 | 3440 |
| CCAAGCATCC | | | 3441 |
| TAAGTGTCTT | | | 3442 |
| GTTTCTAATA | Human microtubule-associated protein 4 mRNA, compl | M64571 | 3443 |
| TTGCTCAGGC | | | 3444 |
| AGGTGAGAGG | | | 3445 |
| AGTAGCCGTG | | | 3446 |
| TACCCAAATA | | | 3447 |
| ATGGCTGGTT | | | 3448 |
| ACTAACACCT | | | 3449 |
| GTTCCCCCGA | | | 3450 |
| ATTCTGGACT | | | 3451 |
| CAAATAAAAG | Human BENE mRNA, partial cds. | U17077 | 3452 |
| TTGTCCTCTG | | | 3453 |
| CACTCACACA | | | 3454 |
| CTGCGGTGCT | | | 3455 |
| ATGCGCAAGG | H.sapiens (xs13) mRNA, 284bp. | Z36785 | 3456 |
| ATGGCAGGTG | | | 3457 |
| TGGCTTCAAG | | | 3458 |
| TGACTTTTCT | | | 3459 |
| TCTTAATGAA | Homo sapiens mRNA for eukaryotic initiation factor | D30655 | 3460 |
| TGTTTCAGTTG | | | 3461 |
| AAACTGATTG | | | 3462 |
| TGTTTGTACA | | | 3463 |
| TACAGGTTTT | | | 3464 |
| TCAACAGCAG | | | 3465 |
| CCACTGCACA | | | 3466 |
| TATTCTCAAT | Human clone 23693 mRNA sequence. | U79254 | 3467 |
| AATCCCTGTG | | | 3468 |
| ACACAGCAAA | | | 3469 |
| ACGAGCTGGA | | | 3470 |
| TACTCGGTTG | | | 3471 |
| ACGTCACCAT | | | 3472 |
| TTCATTAAAA | | | 3473 |
| GAATCATTTA | | | 3474 |
| CAGGCTTTGC | | | 3475 |
| CTGCTAGGAA | | | 3476 |
| CTGCTAGGGG | | | 3477 |
| CTGGGCAGCA | | | 3478 |
| AATGCTTGAT | Human retinoblastoma-binding protein | U35143 | 3479 |

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| | (RbAp46) mRNA | | |
| AATGGCACTT | | | 3480 |
| CTGCAACCTA | | | 3481 |
| GAACCCAAAG | | | 3482 |
| CTCCTTAGAA | | | 3483 |
| ACCTTCAAAA | | | 3484 |
| ACTTGCCATT | H.sapiens RY-1 mRNA for putative nucleic acid bind | X76302 | 3485 |
| GAATTTGTGT | | | 3486 |
| GACACACAGA | | | 3487 |
| GGCAGCACAA | | | 3488 |
| AGAAGCAAGA | | | 3489 |
| ACAGGGGTTC | | | 3490 |
| CCTGAATCTG | | | 3491 |
| CCACTTCAAG | | | 3492 |
| CCAGCTCCTT | | | 3493 |
| GTGCGCAGAG | | | 3494 |
| TTTGTITTTA | Human prolyl 4-hydroxylase alpha (II) subunit mRNA | U90441 | 3495 |
| CCCATTCGGA | | | 3496 |
| GTCTTTCTTG | | | 3497 |
| TTCCAGTAAA | | | 3498 |
| AAAGAATATG | | | 3499 |
| GACTTCTGTC | Human aldehyde dehydrogenase (ALDH8) mRNA, complet | U37519 | 3500 |
| AAATGTTCTG | | | 3501 |
| AACTGCTTTC | | | 3502 |
| CGGGCCGTGC | H.sapiens mRNA for Glyoxalase II. | X90999 | 3503 |
| GGGCTCTGAG | | | 3504 |
| CTACACCAGT | | | 3505 |
| CTCACGCCTG | Homo sapiens Ly-9 mRNA, complete cds. | L42621 | 3506 |
| GTAATAAAAC | | | 3507 |
| TTAGGCAAGT | | | 3508 |
| CTTTTCTTCT | Homo sapiens clone 24498 RNA polymerase II 140 kDa | AF0550 | 3509 |
| TCACAAGCAA | H.sapiens alpha NAC mRNA. | X80909 | 3510 |
| GCCTCTGTCT | | | 3511 |
| TACACTACTG | | | 3512 |
| TAAGTGCCTC | Human B-cell mRNA for a member of the short-chain | D82061 | 3513 |
| GGGGAAATCC | | | 3514 |
| GTGATCAGCT | H.sapiens mRNA for apomucin. | Z48314 | 3515 |
| TACACGTGAG | | | 3516 |
| GAGGAGGAGG | | | 3517 |
| GGGGCCAGGG | | | 3518 |

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| TAAAATTTGT | | | 3519 |
| TTCTATTTTG | Human CD27BP (Siva) mRNA, complete cds. | U82938 | 3520 |
| TTTCTAGTTT | Human mRNA for KIAA0108 gene, complete cds. | D14696 | 3521 |
| GAGGGAAATG | Homo sapiens clone 23701 mRNA sequence. | AF0381 | 3522 |
| GAGCTCTGCG | | | 3523 |
| TGACTGGCAA | | | 3524 |
| GATTTGTGTT | | | 3525 |
| GCTTATAGTC | | | 3526 |
| GAAATCCGCA | Human lysosomal acid alpha- mannosidase mRNA, compl | U68567 | 3527 |
| TGATGTCCAC | | | 3528 |
| TGTAATCTTA | | | 3529 |
| TGCTGAAGAT | | | 3530 |
| TTGTTGGATA | | | 3531 |
| AGAGCCAAGT | | | 3532 |
| GAAGTCGGAA | | | 3533 |
| TGTAGTTTGA | Human RNA polymerase II elongation factor-like pro | U37558 | 3534 |
| GGCTACACCT | Human mRNA for T cell receptor V beta 14 CDR3, par | D32027 | 3535 |
| TAGGTTGTTC | | | 3536 |
| GTGGCATCCG | | | 3537 |
| GGCAGACAAT | | | 3538 |
| TGTTTTTATG | | | 3539 |
| GCACGCGTAA | | | 3540 |
| GCCGAGGAGG | | | 3541 |
| TTGCTCAAGT | | | 3542 |
| GAATCAGGGG | | | 3543 |
| GGCCGAGGAA | | | 3544 |
| AAGTGAGGAG | | | 3545 |
| AGGGTGT,TTT | Homo Sapiens mRNA, partial cDNA sequence for human | AJ0018 | 3546 |
| TACAGTATGT | glutamine synthetase [human, tumorous liver, mRNA | S70290 | 3547 |
| GAGTGAAAGA | | | 3548 |
| CATTTCATAA | Human H ⁺ -ATP synthase coupling factor 6 mRNA, comp | M73031 | 3549 |
| GAGGGAGGAT | | | 3550 |
| GATTTAGCCC | | | 3551 |
| GCCTCCAAGG | Human glyceraldehyde 3-phosphate- dehydrogenase mRN | M28283 | 3552 |
| GCTGTTTTGT | | | 3553 |
| GGAGGGGAGG | | | 3554 |

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| TAATAAAGGG | | | 3555 |
| GTTTCAGGTA | Homo sapiens calcium-ATPase (HK2) mRNA, complete c | M23115 | 3556 |
| GTTACCGAGG | Human (clone 51C-3) 51C protein mRNA, complete cds | L36818 | 3557 |
| GTGGCCACGT | | | 3558 |
| GTGGTGCCTG | | | 3559 |
| CAGATGTGGA | | | 3560 |
| GTTCCAGTGA | | | 3561 |
| GTTTTAAGGC | | | 3562 |
| CAGGGATGTG | | | 3563 |
| TGTCGCTGGG | | | 3564 |
| GTAAGATTTG | | | 3565 |
| CAAGTTCTTT | | | 3566 |
| TAGATGTGAT | | | 3567 |
| CAAAATTCCT | | | 3568 |
| TACAAAGCAT | | | 3569 |
| ACGTTAACCT | | | 3570 |
| TACTCTTGGG | | | 3571 |
| CAACAAAAAA | | | 3572 |
| TACCCATCAA | | | 3573 |
| CAAGGTAAAA | | | 3574 |
| TACCATCATA | | | 3575 |
| CTGTGCTCGG | Human mRNA for mitochondrial short-chain enoyl-CoA | D13900 | 3576 |
| AATCTTGCAA | | | 3577 |
| GCTCACGCCT | | | 3578 |
| GTTGCTCTAT | | | 3579 |
| TACCATCAAC | | | 3580 |
| CACAACCTCC | H.sapiens SH3GLP3 pseudogene, 5' end. | X99662 | 3581 |
| CACCACCACA | | | 3582 |
| GTGTGAAATA | Human mRNA for RanBP2 (Ran-binding protein 2), com | D42063 | 3583 |
| GTTGGGACAT | | | 3584 |
| TAATAAAAGG | | | 3585 |
| TAACCGTGCG | | | 3586 |
| TAACCCACTG | | | 3587 |
| CACTAGTCCC | | | 3588 |
| CACTCAGTAA | | | 3589 |
| CACTCTATCC | | | 3590 |
| CAAGTAATGA | | | 3591 |
| GTATCTATGC | | | 3592 |
| GTGCTTATAA | Human protein tyrosine phosphatase mRNA, complete | L77886 | 3593 |
| GGGGAGGGGG | Human mRNA for upstream binding | X53461 | 3594 |

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| | factor (hUBF). | | |
| GGGCTGGTCT | | | 3595 |
| CCCCAGGGAG | | | 3596 |
| GGGAGGATTA | | | 3597 |
| GTGAAACCGC | | | 3598 |
| CCCCGTACAC | | | 3599 |
| GACATAGTAA | | | 3600 |
| GTCGGGCCTC | H.sapiens mRNA for adult folate binding protein. | X62753 | 3601 |
| GTCCTGCAGA | | | 3602 |
| GGCTTGGCCC | | | 3603 |
| GTCACACTGG | | | 3604 |
| CCCCTTGGAT | | | 3605 |
| AACCAGGGAG | | | 3606 |
| AAACTGCATT | | | 3607 |
| GGCCGAGGGA | | | 3608 |
| GGCCGTGCTG | | | 3609 |
| AAATCAAGTC | | | 3610 |
| AAAGCGTAAA | Human interferon-gamma receptor mRNA, complete cds | J03143 | 3611 |
| GGGTTTTTAA | Human FUSE binding protein 3 (FBP3) mRNA, partial | U69127 | 3612 |
| CCCGACTCCT | | | 3613 |
| GTGAGACCCC | Human clone 2C2 Cri-du-chat critical region mRNA, | U10510 | 3614 |
| AAACATTAAA | Human mRNA for enteric smooth muscle gamma-actin. | X16940 | 3615 |
| GGTGACCGTC | Human cyclophilin-like protein mRNA, partial cds. | U37221 | 3616 |
| AAACTCACGC | | | 3617 |
| GATAGATGATG | | | 3618 |
| AAACCAGGGC | | | 3619 |
| GGCTGGGGCC | Human mRNA for medullasin (leukocyte (neutrophil)) | X05875 | 3620 |
| GGTAGCCCAC | | | 3621 |
| AAAGACAGTG | | | 3622 |
| CCTGTGTGTG | | | 3623 |
| GTGTTCCCCA | | | 3624 |
| GTGGCACGCG | | | 3625 |
| GTGTTCCCAT | | | 3626 |
| GTGGAACCCC | | | 3627 |
| GTATCTTCAC | | | 3628 |
| GTGTGCTGGC | Human clone pJS3 interferon gamma receptor accesso | U05877 | 3629 |
| TAACGTCTGC | | | 3630 |
| GTGCTGATCT | | | 3631 |

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| GTGCATTTTCG | | | 3632 |
| GTGAACCTCT | | | 3633 |
| GTGGCGTGCA | | | 3634 |
| GTGAACCCCT | | | 3635 |
| GTGGCGCATA | | | 3636 |
| CCCACGTCCT | | | 3637 |
| GTGCGCTAAG | | | 3638 |
| GTGCCACGGC | | | 3639 |
| CCATTGCATT | Human bfr mRNA for fibroblast growth factor (FGR) | X56191 | 3640 |
| GTGAAAACCT | | | 3641 |
| GTGCCAGCCC | | | 3642 |
| GTGCCTGTGC | | | 3643 |
| CCAGTAGAAG | | | 3644 |
| GTCACACCAC | | | 3645 |
| GTGAACCCCC | | | 3646 |
| GTGCGGAAGG | | | 3647 |
| GGAAGGACAG | H.sapiens mRNA for vacuolar proton ATPase, subunit | X71490 | 3648 |
| GTGAACCCCA | Human HepG2 3' region Mbol cDNA, clone hmd3c03m3. | D17194 | 3649 |
| GTGCTGGTCC | | | 3650 |
| GTGGAAACTG | | | 3651 |
| CATATCCTGA | HP1Hs alpha=25 kda chromosomal autoantigen [human, | S62077 | 3652 |
| CCATCGTCCT | | | 3653 |
| TTGTAAATCG | | | 3654 |
| TTCTGTGTAT | | | 3655 |
| AAAAACATTC | | | 3656 |
| ACTGGTACGT | | | 3657 |
| TTTTTATCCA | | | 3658 |
| TTTGTGCTT | | | 3659 |
| TTGGAACAAT | | | 3660 |
| TTTGGGGTTT | | | 3661 |
| TGCACTGAAT | | | 3662 |
| TGCAATAAGA | | | 3663 |
| AGGATATCCA | | | 3664 |
| TTTCTGTGTA | | | 3665 |
| TTGGGGTTTG | | | 3666 |
| TAGGGCTCTC | | | 3667 |
| TTTCCAAGAG | Human HF.12 gene mRNA. | X07290 | 3668 |
| GACCAGCTGG | Human apM2 mRNA for GS2374 (unknown product specif | D45370 | 3669 |
| TTTATGGGTT | | | 3670 |
| TTGTTTGTTT | | | 3671 |
| AGGCCTCCCC | | | 3672 |

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| AGGCCTGGGC | | | 3673 |
| AGGCTGCCCA | | | 3674 |
| TTTGCGGCAG | | | 3675 |
| TTTGTTGACT | | | 3676 |
| TTTTCTTTAG | Human mRNA for KIAA0347 gene, complete cds. | AB0023 | 3677 |
| TTTTGTATTT | | | 3678 |
| AGGGAGTGTC | | | 3679 |
| AGGGTTTCTC | | | 3680 |
| TTGTTGAAGC | | | 3681 |
| AGTGTGTTGC | | | 3682 |
| TTTCTGAAAA | | | 3683 |
| AAAGAAGCTC | | | 3684 |
| TGGACAAGTC | | | 3685 |
| TGGACATCAT | | | 3686 |
| ACTTAGGCTT | | | 3687 |
| TGGCAGCTTT | | | 3688 |
| TGCTTATTGA | | | 3689 |
| TGGCTGAGCA | | | 3690 |
| ACTTGATAAA | | | 3691 |
| ACTTTATTAG | | | 3692 |
| TGCTCTTTCC | | | 3693 |
| TGCTCAACAG | | | 3694 |
| TGTCAGAATT | | | 3695 |
| TGCATCTGGT | H.sapiens mRNA for BiP protein. | X87949 | 3696 |
| TGCGTCACCG | | | 3697 |
| AGCCTCGGGC | | | 3698 |
| TGCCCTTCAG | | | 3699 |
| TCTTTTCAA | | | 3700 |
| TGCCCTCAAG | | | 3701 |
| AGCCAGATCA | | | 3702 |
| TTCCAGATGG | | | 3703 |
| TTCAATACAC | | | 3704 |
| TGTGTTGAAA | | | 3705 |
| TGCCCTCAGC | | | 3706 |
| TGTTGTTGAG | | | 3707 |
| TTAGTCAGGT | | | 3708 |
| TTAGGTTGTC | | | 3709 |
| TTAGGAGGGT | | | 3710 |
| TTAGAGCCTA | | | 3711 |
| AAACGACCTC | | | 3712 |
| TTCTGCATCC | | | 3713 |
| AAAAGGTTAT | | | 3714 |
| TCATCATCAG | | | 3715 |
| TGAAGGGTAT | | | 3716 |
| GAAATGTAAG | | | 3717 |

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| TGACTGTCAC | | | 3718 |
| AACCCAGGAG | Human clone 23618 mRNA sequence. | AF0071 | 3719 |
| CGCACCATTG | GCN5-like 1=GCN5 homolog/putative regulator of tra | S82447 | 3720 |
| TGAAAAGCTT | N8=tumor expression-enhanced gene [human, NCI H-69 | S82081 | 3721 |
| TCTCTACTCT | | | 3722 |
| TCCGTGGTTG | Homo sapiens neuronal tissue-enriched acidic prote | AF0396 | 3723 |
| GTGGCGGGCG | Homo sapiens malignancy-associated protein mRNA, p | AF0414 | 3724 |
| TATTTTGTTA | Homo sapiens cdc14 homolog mRNA, complete cds. | AF0003 | 3725 |
| TGTCCTGGTT | Human wild-type p53 activated fragment-1 (WAF1) mR | U03106 | 3726 |
| TATTTTCTTT | H.sapiens polyA site DNA sequence. | Z24749 | 3727 |
| TTTCAGAGAG | Homo sapiens signal recognition particle subunit 9 | U20998 | 3728 |
| TGCCCTTCAA | | | 3729 |
| GTCTATGCCT | | | 3730 |
| TACTGGCCGC | | | 3731 |
| TATTTAAACA | | | 3732 |
| GCTTTT TAGA | Human non-histone chromosomal protein HMG-14 mRNA, | J02621 | 3733 |
| TAGCTGTCTT | | | 3734 |
| ATTCTGTCAA | | | 3735 |
| TATCTGCCAA | | | 3736 |
| AAGAAGCAAG | | | 3737 |
| ATGGTTCTCA | | | 3738 |
| ATTACAGCCA | | | 3739 |
| ATTA ACTTAT | | | 3740 |
| TCAGTACAGA | | | 3741 |
| TCAGTTCTTG | | | 3742 |
| ATGTCTTTTC | Human insulin-like growth factor binding protein 4 | M62403 | 3743 |
| TGCTGTGCAT | Homo sapiens dead box, X isoform (DBX) mRNA, alter | AF0009 | 3744 |
| TCAGAAGTTT | | | 3745 |
| TCCTTGGACC | Human proline dehydrogenase/proline oxidase (PRODH | U82381 | 3746 |
| ATTGATCAAT | | | 3747 |
| TTGTCCATAT | | | 3748 |
| TCTGCGCATC | | | 3749 |
| GGAGGCCGAG | | | 3750 |
| ATAAAACATT | | | 3751 |
| ATAATAAAAG | Human cytokine (GRO-gamma) | M36821 | 3752 |

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| | mRNA, complete cds. | | |
| TTGCTTGAGC | | | 3753 |
| ATACTAGTGG | | | 3754 |
| TCTCCGTACA | | | 3755 |
| GGCCTGCTGC | | | 3756 |
| TTCCCTGTGT | | | 3757 |
| TTCCAGCTTA | | | 3758 |
| CACTACACGG | Human rapamycin- and FK506-binding protein, comple | M75099 | 3759 |
| TGATCGCGGC | | | 3760 |
| ATCTGTTTAT | | | 3761 |
| TGGGCAGCTG | | | 3762 |
| TCATTATTTA | | | 3763 |
| TCATTTTGGA | | | 3764 |
| TGTCTCAAAA | | | 3765 |
| ACTCTAGACA | | | 3766 |
| TCTAGCATTT | | | 3767 |
| ATGAACTCCT | | | 3768 |
| TTCAGTGCTA | | | 3769 |
| TGTCTGGTTG | | | 3770 |
| ATCGTGCGCT | | | 3771 |
| ATCCAAATTT | | | 3772 |
| ATCATAGACG | | | 3773 |
| TTAAATCGTG | | | 3774 |
| TTGTTACATC | Human mRNA for phosphoribosypyrophosphate syntheta | D61391 | 3775 |
| TCCCTTAAGC | | | 3776 |
| GCCCCAGCCA | | | 3777 |
| CACTGTGACC | | | 3778 |
| AAGCCCTACA | | | 3779 |
| GCCAGGGCCA | | | 3780 |
| CATAGCCTGG | | | 3781 |
| AATAAAGGTG | | | 3782 |
| CATCCCGTGA | Human leukotriene A-4 hydrolase mRNA, complete cds | J03459 | 3783 |
| CAGGGTCCCC | | | 3784 |
| CATTTCAATA | | | 3785 |
| GCCCCAGCTG | Homo sapiens N-methyl-d-aspartate receptor (NR1-2) | L13267 | 3786 |
| GAGCAAAGGA | | | 3787 |
| GAGCACCTCC | | | 3788 |
| CAGCTGCTCC | | | 3789 |
| CAGCACAGAC | | | 3790 |
| GCCGAGGAAA | | | 3791 |
| CAGTGGGTGG | Human mRNA for UDP-galactose transporter related i | D87989 | 3792 |

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| CCACTCTCAG | | | 3793 |
| ACACAAGTCG | | | 3794 |
| CCAGCAGAAG | | | 3795 |
| GCAACTGTGA | | | 3796 |
| GCAAGCCATC | | | 3797 |
| GCACAGGCCA | | | 3798 |
| GCCAGAACAG | | | 3799 |
| GCACCCAACA | Human prostate carcinoma tumor antigen (pcta-1) mR | L78132 | 3800 |
| CACTGCCTTG | | | 3801 |
| CTTGGGATGT | | | 3802 |
| CCACCTTTCC | | | 3803 |
| CCACAGCTGT | | | 3804 |
| GCAGTGCCCA | | | 3805 |
| CCAATTTACA | | | 3806 |
| GAGAGAAAAT | | | 3807 |
| ACAATATCGA | | | 3808 |
| CTGCTGGAGG | | | 3809 |
| CACTGTGCCT | | | 3810 |
| ATGTTTTGCA | | | 3811 |
| ATGTTGCTGA | | | 3812 |
| GCACCCTCAG | Human RGP3 mRNA, complete cds. | U27655 | 3813 |
| ATGGGGGGCA | | | 3814 |
| CAAAACAGGC | | | 3815 |
| ATGGCTAAGC | | | 3816 |
| TGGAACAGGA | H.sapiens mRNA for TGIF protein. | X89750 | 3817 |
| CTGCTAAGGT | | | 3818 |
| GCAGAGATGG | | | 3819 |
| GCCAGCCCAT | | | 3820 |
| ACTGTATTTT | | | 3821 |
| GCCCATTGCT | | | 3822 |
| CAAGCCATCC | | | 3823 |
| GCGGGAGCGG | Human mRNA for KIAA0224 gene, complete cds. | D86977 | 3824 |
| ACAGATGTTG | Human mRNA for proteasome subunit p42, complete cd | D78275 | 3825 |
| CACTGCATAT | Human phosphorylase kinase (PSK-C3) mRNA, complete | M31606 | 3826 |
| GCCGGCCTTT | | | 3827 |
| GCCTCAGTTC | | | 3828 |
| ACCTATAAGT | | | 3829 |
| CTGTCCGTAC | | | 3830 |
| ATTTCTGCTG | | | 3831 |
| GCCTCGGCCT | Homo sapiens putative DDB p127-associated protein | AF0359 | 3832 |
| CCCCTGCAC | | | 3833 |

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|------------|--|--------|------|
| CACCTGTCCT | | | 3834 |
| GGGACCCCGG | Human chloride channel protein (CLCN7) mRNA, parti | U88844 | 3835 |
| CACAAGATGA | | | 3836 |
| GGGGCTGTGG | Human TFIIIC Box B-binding subunit mRNA, complete | U02619 | 3837 |
| GAGGGAGTTC | | | 3838 |
| GCGAGACCCT | | | 3839 |
| GCCTCCGAGA | | | 3840 |
| GAATATGGCT | | | 3841 |
| CTTCTGTCTC | | | 3842 |
| CTCGTTAAGA | | | 3843 |
| CTCCCAGGTC | H.sapiens mRNA for M-phase phosphoprotein, mpp6. | X98263 | 3844 |
| AAAGTCAGAA | Human cytochrome bc-1 complex core protein II mRNA | J04973 | 3845 |
| AATAAAGTTG | | | 3846 |
| CTCTAGTCCA | | | 3847 |
| ACTCACGATT | | | 3848 |
| GACTGGAAC | | | 3849 |
| GAGAATCTGC | | | 3850 |
| CAAATGAGGA | | | 3851 |
| CAATGTGTTA | H.sapiens mRNA for NADH dehydrogenase. | X81900 | 3852 |
| CTTTTGGTTT | Human p76 mRNA, complete cds. | U81006 | 3853 |
| CATTAAAGGG | | | 3854 |
| TGCTGAATCA | | | 3855 |
| AAGTACTTCA | | | 3856 |
| GCCCGCAGGT | | | 3857 |
| CCCATCGTTC | | | 3858 |
| ACCAAATTAA | Homo sapiens TRAIL receptor 2 mRNA, complete cds. | AF0162 | 3859 |
| ACATTTCCAA | | | 3860 |
| CTGCTGTCCC | | | 3861 |
| GACAACAGTC | H.sapiens (xscad) mRNA, 340bp. | Z36852 | 3862 |
| GAGAAACCTT | | | 3863 |
| CTGCCTGGCA | Homo sapiens X-ray repair cross-complementing prot | AF0355 | 3864 |
| GAAGCCAGGA | | | 3865 |
| GCCTGTTTGG | Homo sapiens phenol UDP-glucuronosyltransferase (U | J04093 | 3866 |
| GCTGCACCGG | | | 3867 |
| GACGTAGCGG | | | 3868 |
| CTGAGGGCCG | | | 3869 |
| CTTGTGTGTA | Human mRNA for KIAA0059 gene, complete cds. | D31883 | 3870 |

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| GAATCATTTT | | | 3871 |
| CTGCTGCTGG | | | 3872 |
| GAGTTTTTAA | | | 3873 |
| CCCTCGGAAA | | | 3874 |
| GAGGGATTTC | | | 3875 |
| CCCTCATCCC | | | 3876 |
| GAAGAGGCCT | | | 3877 |
| GAGGGTATAC | Human mRNA for transcription factor TFE3 (partial) | X51330 | 3878 |
| CCCGTCCGGG | | | 3879 |
| GAAAACATTC | | | 3880 |
| CCCTCTTTGG | | | 3881 |
| GAAGCAAAAA | | | 3882 |
| CCCATATTTT | Human L-isoaspartyl/D-aspartyl protein carboxyl me | M93008 | 3883 |
| GATGACTTGC | | | 3884 |
| CCCATAATCC | Homo sapiens 15S-lipoxygenase mRNA, complete cds. | U78294 | 3885 |
| GATGGTCAGT | | | 3886 |
| CTGGGACTGC | | | 3887 |
| CCCGGTGTGT | | | 3888 |
| CCTACAGATA | | | 3889 |
| GAATACCTTC | | | 3890 |
| GAAGCAATAA | Human RNA sequence of the human DS glycoprotein al | X00033 | 3891 |
| CGGTTTGCA | | | 3892 |
| CGGGAGCACC | | | 3893 |
| CCTCTGGAGG | | | 3894 |
| GGAGGGATCA | Homo sapiens mRNA fragment. | L10140 | 3895 |
| TTGTCTGCCT | | | 3896 |
| GTGAAGTCTT | Homo sapiens clone 24551 mRNA sequence. | AF0550 | 3897 |
| GAACAATTAC | | | 3898 |
| TACTTGTGTG | Homo sapiens clone 23742 mRNA, partial cds. | AF0352 | 3899 |
| TAACAGCCAG | Homo sapiens MAD-3 mRNA encoding I κ B-like activity | M69043 | 3900 |
| CCGGACCTGT | | | 3901 |
| CCGCTGCACT | | | 3902 |
| GAAGAAAACA | H.sapiens mRNA for mitochondrial transcription ter | Y09615 | 3903 |
| GAAAAAATGG | | | 3904 |
| GTCTTGAAGC | | | 3905 |
| AGGTGGGCAA | | | 3906 |
| AGTACGAATG | | | 3907 |
| AGGATGTACA | Homo sapiens DEME-6 mRNA, partial | AF0071 | 3908 |

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| | cds. | | |
| GTTCCCTGGG | | | 3909 |
| GTTATAAGAT | Human deleted in split hand/split foot 1 (DSS1) mR | U41515 | 3910 |
| GTGCAGGGAG | | | 3911 |
| GTCAGAACTT | | | 3912 |
| GGAGGAAGTG | | | 3913 |
| AGGGAAAAAA | | | 3914 |
| GGAGCAGGAC | | | 3915 |
| GCTGTAGTCC | | | 3916 |
| GGCCCAGGCC | Human aldehyde dehydrogenase mRNA, complete cds. | M77477 | 3917 |
| GGAGCACTGT | | | 3918 |
| TTGGGGTTCC | | | 3919 |
| GCTTGTTCTC | Human mRNA for heparan sulfate proteoglycan (glypi | X54232 | 3920 |
| ACATAAGATC | | | 3921 |
| GGCTTTGGTC | | | 3922 |
| GGCTTTGGTG | | | 3923 |
| GGAAGTGGCC | | | 3924 |
| GGCTTTTATG | | | 3925 |
| CGATCAGTTT | | | 3926 |
| GGGAGGGAAG | Human mRNA for KIAA9001 gene, complete cds. | D42040 | 3927 |
| ACCTTTGCGA | | | 3928 |
| CCTTGTCCTC | H.sapiens mRNA for GM2 activator protein. | X62078 | 3929 |
| AGGAAAAAAA | | | 3930 |
| AGTAACGTGT | | | 3931 |
| GGGCAGGGGA | | | 3932 |
| GCTGGGCTGG | | | 3933 |
| GACATATGTA | H.sapiens coxVIIb mRNA for cytochrome c oxidase su | Z14244 | 3934 |
| GGAGAGTACA | | | 3935 |
| GGAGATGGAG | | | 3936 |
| ACTGGGGAAT | | | 3937 |
| CGCCGCCGGT | | | 3938 |
| GGACATCAAG | | | 3939 |
| TTTGTCTGTG | | | 3940 |
| TTTGTAGATG | Human HepG2 3' region Mbol cDNA, clone hmd3c06m3. | D17196 | 3941 |
| ACTGCTGAAC | Homo sapiens secretory carrier membrane protein (S | AF0050 | 3942 |
| ACTTTGATGA | | | 3943 |
| GGCAGCGCCC | | | 3944 |
| TTGTGGGATC | | | 3945 |

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| GCTTTGGGAT | | | 3946 |
| TTGGTGGAGG | | | 3947 |
| TTGCGTGCTG | | | 3948 |
| GCCGCTACTT | | | 3949 |
| TGGGGGCACC | Homo sapiens I-Rel mRNA, complete cds. | M83221 | 3950 |
| GTCTTGAAC | Human asparagine synthetase mRNA, complete cds. | M27396 | 3951 |
| TGGGCCCCGTG | | | 3952 |
| AGACAATTTT | Human breast cancer cytosolic NADP(+)-dependent ma | U43944 | 3953 |
| CGGTCTTATG | Human mRNA for serine/threonine protein kinase, co | D86550 | 3954 |
| ACCTGGTGCC | | | 3955 |
| GGCACACCTT | | | 3956 |
| TGCCTGTAGT | Human primary Alu transcript. | U67823 | 3957 |
| TCCCCATTAA | | | 3958 |
| TCATCTCCCT | | | 3959 |
| GGCCGTGTCC | | | 3960 |
| AGCACTTTTG | Human FEZ2 mRNA, partial cds. | U60061 | 3961 |
| GGCCTGTGGA | | | 3962 |
| AGCCTGGGCC | | | 3963 |
| AGCTGGGATG | | | 3964 |
| GCTTGCTGGC | | | 3965 |
| CCTCTTTCAG | | | 3966 |
| CAGCATCCCC | | | 3967 |
| ATAGTCTGTT | | | 3968 |
| CTGAGGGTGG | | | 3969 |
| GGATTTGGGC | | | 3970 |
| CTAAAAGGAG | Human autoimmune antigen small nuclear ribonucleop | M15919 | 3971 |
| AAGAATTTGA | | | 3972 |
| GCGGCTTTCC | Homo sapiens cDNA homologous to Yeast SCO1 & SCO2 | AL0216 | 3973 |
| ATATGATCAT | Human ADP-ribosylation factor-like protein 4 mRNA, | U73960 | 3974 |
| GGGCTACGGA | | | 3975 |
| ATCACCCCCT | | | 3976 |
| ATGACACTCA | | | 3977 |
| ATCAGTGTGC | | | 3978 |
| CAGGGGCTGG | | | 3979 |
| AGGTGGCCAA | | | 3980 |
| TTTGGTCTTT | | | 3981 |
| GCCTTAAAAA | | | 3982 |
| GCTGTAATCC | Human clone 30849 defective mariner transposon Hsm | U92026 | 3983 |

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| ACTGACTATC | H.sapiens G9 gene encoding sialidase. | X78687 | 3984 |
| ACCTGTATCC | Human 1-8U gene from interferon-inducible gene fam | X57352 | 3985 |
| CTCACTTTT | Human NF-IL6-beta protein mRNA, complete cds. | M83667 | 3986 |
| ATGAATTAGC | | | 3987 |
| GGCACAATCA | | | 3988 |
| CCTCCGGCCA | | | 3989 |
| AAGGCCTCGG | | | 3990 |
| AAGAACCAAG | Human autonomously replicating sequence (ARS) mRNA | L08436 | 3991 |
| ATGCCTATTT | | | 3992 |
| GCTGAGGGCT | | | 3993 |
| ATGCTTGCTT | | | 3994 |
| ATCGCACCAC | | | 3995 |
| ATAGAGGCAA | Human mRNA for KIAA0026 gene, complete cds. | D14812 | 3996 |
| GGAGGCAGGG | | | 3997 |
| GGACCCTCTC | Human clone 23764 mRNA sequence. | AF0071 | 3998 |
| AATAAAATTA | Human lymphotactin precursor mRNA, complete cds. | U23772 | 3999 |
| CCTGGGTCCC | insulin receptor [human, familial insulin resistan | S70454 | 4000 |
| GCTGGGATCA | | | 4001 |
| GGATTGGCCT | | | 4002 |
| GGAAGTGCCA | | | 4003 |
| ATACTGCTGC | Human CUL-2 (cul-2) mRNA, complete cds. | U83410 | 4004 |
| AAGGAGTCCC | | | 4005 |
| GCTGAGAATA | | | 4006 |
| CCCTCAATCC | Human Liver mRNA for interferon-gamma inducing fac | D49950 | 4007 |
| GCTCAGATCG | | | 4008 |
| CTATCAGGTA | | | 4009 |
| CAGTCCCCCT | Human mRNA for KIAA0153 gene, partial cds. | D63487 | 4010 |
| CATTCCTCCT | H.sapiens mRNA for emerin. | X82434 | 4011 |
| CAGGGGTGAC | | | 4012 |
| GGGAGCCGAG | Human mRNA for KIAA0169 gene, partial cds. | D79991 | 4013 |
| GCTTATGTTA | | | 4014 |
| AAGACCTACA | | | 4015 |
| AAACGCGGCC | | | 4016 |
| AAGACTGAAG | | | 4017 |
| AAATAAAAAA | | | 4018 |

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| GGCTCACTTT | | | 4019 |
| AACAGTGTGC | | | 4020 |
| AAAAGAAGTT | | | 4021 |
| AAAAGATACT | | | 4022 |
| AACAACAGTG | | | 4023 |
| AACGCGGGCC | | | 4024 |
| AAGCTCTGTG | | | 4025 |
| TTTTCTGAGT | | | 4026 |
| AAAATAAATT | | | 4027 |
| AAATGTGAAT | | | 4028 |
| AACCTGTTTT | Human alcohol dehydrogenase class III (ADH5) mRNA, | M29872 | 4029 |
| AAATCAGGAA | | | 4030 |
| AAGTAGCTGG | | | 4031 |
| AAAACGGCA | | | 4032 |
| AAGGTAGATG | Homo sapiens 5,10-methenyltetrahydrofolate synthet | L38928 | 4033 |
| TTTGAACCCT | | | 4034 |
| TTTCTTTTTG | | | 4035 |
| AAATCCTGTG | | | 4036 |
| AAAACATTAA | | | 4037 |
| GGCCGGGTGG | | | 4038 |
| GGAGCTGTCT | | | 4039 |
| TGGTACTTCT | | | 4040 |
| GTGCAAAATG | | | 4041 |
| AACTGCGGCA | | | 4042 |
| TTCATCTCTT | Human pyruvate carboxylase precursor, mRNA, nuclea | U30891 | 4043 |
| AAGAAATGCA | | | 4044 |
| TACCAAGACC | H.sapiens mRNA for beta-COP. | X82103 | 4045 |
| TACGTCCACG | | | 4046 |
| TTATATTGCC | | | 4047 |
| TAGCAGAGGC | | | 4048 |
| TAGCCCCAGC | Human variant urokinase plasminogen activator rece | U09347 | 4049 |
| TGTTACAGCC | | | 4050 |
| TCAACTGAAG | | | 4051 |
| AAGTTTATAG | | | 4052 |
| TGTGCTGAGA | | | 4053 |
| TTCCCAGGAG | | | 4054 |
| TCCCTGGCAT | | | 4055 |
| TCTGCACTGA | | | 4056 |
| TCTGTGCTCA | | | 4057 |
| AAGAACATTG | H.sapiens mRNA for ATP-citrate lyase. | X64330 | 4058 |
| AATATGGGTG | Human tetratricopeptide repeat protein (tpr2) mRNA | U46571 | 4059 |

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| TGGGTGAGCC | Homo sapiens cathepsin B mRNA, complete cds. | L16510 | 4060 |
| AATATGGTAC | | | 4061 |
| TGAGCAAGCC | | | 4062 |
| TGCACACACA | Homo sapiens (clone KT4) bone morphogenetic protei | L35278 | 4063 |
| TGCACCTTGG | Human cdc2-related protein kinase mRNA, complete c | M68520 | 4064 |
| TGCTCTCTCT | | | 4065 |
| TGGAGAGTCG | | | 4066 |
| TCATTTTTTT | | | 4067 |
| AAGTGGCAAG | | | 4068 |
| TTGGTCCCTC | | | 4069 |
| TTGGTAAATG | | | 4070 |
| GGGCATCTCT | Human mRNA for histocompatibility antigen HLA-DR (| V00523 | 4071 |
| TTGGGGTTCT | | | 4072 |
| AAGATGGCCC | Human mRNA for non-erythropoietic porphobilinogen | X04808 | 4073 |
| GGTGCTCCCT | | | 4074 |
| AAGTGGAGGA | | | 4075 |
| AACGTGCCAG | | | 4076 |
| GGTGGTTGCT | | | 4077 |
| TTGACCAGGC | Human protease-activated receptor 3 (PAR3) mRNA, c | U92971 | 4078 |
| TTGAAGAAAA | | | 4079 |
| GTTTGCAAGT | | | 4080 |
| TCTGACCACC | | | 4081 |
| TTTCACTCCT | | | 4082 |
| GTGGCCTACT | | | 4083 |
| AAGTGGCTGG | | | 4084 |
| GTGGCGCACG | | | 4085 |
| GTGGGGGGAG | | | 4086 |
| GTTATTGAGG | | | 4087 |
| AAGCCGGCCC | | | 4088 |
| GTTGTAAATA | | | 4089 |
| AAGTTGAATT | | | 4090 |
| AACTCCCGTG | H.sapiens (xs163) mRNA, 390bp. | Z36815 | 4091 |
| GTTGTGAAGA | | | 4092 |
| GTTTAGAGGG | | | 4093 |
| TTCTAACATA | Human mRNA for Na/K-ATPase beta subunit. | X03747 | 4094 |
| TTCTTTTCAT | Human protein synthesis factor (eIF-4C) mRNA, comp | L18960 | 4095 |
| CTCAACAGCA | Human translation initiation factor 3 47 kDa subun | U94855 | 4096 |

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| GGCCCGGCTT | | | 4097 |
| TAGACTTATT | Human mitochondrial aspartate aminotransferase mRN | M22632 | 4098 |
| GTTGGGAAGA | | | 4099 |
| GGTGTGAGCC | Human INS-1 winged-helix homolog mRNA, complete cd | U83113 | 4100 |
| GGCCAGGTGG | Human mRNA for KIAA0047 gene, partial cds. | D38554 | 4101 |
| GCTAAGACTT | | | 4102 |
| AATAGCTCAG | | | 4103 |
| GAAGGAAGAA | Human cyclin-dependent protein kinase mRNA, comple | U79269 | 4104 |
| AGGCCAAGGG | | | 4105 |
| ATTGGCTGGG | protein phosphatase 2C alpha [human, teratocarcino | S87759 | 4106 |
| ATTCCAATCT | Human mRNA for KIAA0034 gene, complete cds. | D21260 | 4107 |
| ATCCGGGGAG | Homo sapiens RCL (Rcl) mRNA, complete cds. | AF0401 | 4108 |
| AAATACAGCA | | | 4109 |
| TGTTAATGTT | | | 4110 |
| AAGAAGCAGG | | | 4111 |
| GATCACAGTT | Human mRNA for lactate dehydrogenase B (LDH-B). | Y00711 | 4112 |
| TAGTTGAAGT | Human mitochondrial ubiquinone-binding protein mRN | M22348 | 4113 |
| AGCACTGCAG | | | 4114 |
| AAAAAGCAGA | Human superoxide dismutase (SOD-1) mRNA, complete | K00065 | 4115 |
| TTTACAGCTG | Human diacylglycerol kinase zeta mRNA, alternative | U94905 | 4116 |
| TTACTAAATG | | | 4117 |
| TTAATAGTGG | | | 4118 |
| TGTGTTGTCA | Human mRNA for NAD-dependent methylene tetrahydrof | X16396 | 4119 |
| TCAGTTTGGA | Human palmitoyl protein thioesterase mRNA, complet | U44772 | 4120 |
| TCTCTGCAAA | | | 4121 |
| GCCAAGGGCC | | | 4122 |
| GTGGTGGGCG | | | 4123 |
| CCACCTAATT | | | 4124 |
| CAACATTCCT | Human D-dopachrome tautomerase mRNA, complete cds. | U49785 | 4125 |
| ATTGTGAGGG | | | 4126 |
| ATTCAGCACC | | | 4127 |
| ATGGCAGGAG | | | 4128 |
| TGCTGCTTGA | | | 4129 |

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| GGGGTCAGGG | | | 4130 |
| TCAGAAAGGTG | | | 4131 |
| ACGGCTCCGA | | | 4132 |
| TTGCTAGAGG | | | 4133 |
| TTATGGGGAG | Human transformation-sensitive protein (IEF SSP 35 | M86752 | 4134 |
| TGGTGCAGCA | | | 4135 |
| TGCCATCTGT | | | 4136 |
| GCACCTAATT | | | 4137 |
| GTTTAAATCG | Human mRNA for proteasome subunit HC3. | D00760 | 4138 |
| TCAAATGCAT | Human nuclear ribonucleoprotein particle (hnRNP) C | M16342 | 4139 |
| GAAGGCATCC | Human immunodeficiency virus tat transactivator bi | M34079 | 4140 |
| CAAGTTAGTG | | | 4141 |
| ACTACAAATA | | | 4142 |
| AACTAATACT | | | 4143 |
| TAAGTGGAAT | | | 4144 |
| GGGCTCACCT | | | 4145 |
| TACCAGTGTA | Human mitochondrial matrix protein P1 (nuclear enc | M22382 | 4146 |
| AAGAGTTACG | | | 4147 |
| GAATCCAACT | | | 4148 |
| CTTGAGCAAT | Human immunophilin (FKBP52) mRNA, complete cds. | M88279 | 4149 |
| CTCATAGCAG | | | 4150 |
| CGCTGTGTGC | Human mRNA for alternative splicing product of glu | D13287 | 4151 |
| CCTGTAATCT | Human epidermal growth factor receptor (HER3) mRNA | M34309 | 4152 |
| CCGGCGCGTG | | | 4153 |
| CCGTCATCCT | H.sapiens mRNA for Not56-like protein. | Y09022 | 4154 |
| ACTGGCGAAG | Human hLON ATP-dependent protease mRNA, nuclear ge | U02389 | 4155 |
| ACAGTCTTGC | | | 4156 |
| TGATGTTTGA | Human mRNA for KIAA0058 gene, complete cds. | D31767 | 4157 |
| CTTCTGCTGG | | | 4158 |
| ACCTTGTGCC | Human L-iditol-2 dehydrogenase mRNA, complete cds. | L29008 | 4159 |
| TTTTGGGGGC | | | 4160 |
| TTTCTGTATG | | | 4161 |
| TCACAGCTGT | | | 4162 |
| ATTATTTTTC | Human ribosomal protein L7 (RPL7) | L16558 | 4163 |

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| | mRNA, complete c | | |
| CTGTGAGCCA | | | 4164 |
| TTCCTCCACC | | | 4165 |
| GTGGACCCTG | | | 4166 |
| GGTAGCTCAG | | | 4167 |
| GGGCGGGGGC | Human DNA polymerase delta mRNA, complete cds. | M81735 | 4168 |
| GGCCCTCTGA | Human peptidyl-prolyl isomerase and essential mito | U49070 | 4169 |
| GCCTTGGCCC | | | 4170 |
| GTTGTGGCCA | | | 4171 |
| GCACAAGAAG | | | 4172 |
| TCTCCCTTCA | | | 4173 |
| CAGCCTCCCT | Human uroporphyrinogen III synthase mRNA, complete | J03824 | 4174 |
| CAGAAGAGGC | H.sapiens mRNA for DGCR6 protein. | X96484 | 4175 |
| AGCCACTGCG | | | 4176 |
| AAAGTTCTCA | | | 4177 |
| TTTTGAAGCA | H.sapiens GENX-5624 mRNA, 3' UTR. | X81895 | 4178 |
| AAACACTCTT | H.sapiens OXA1Hs mRNA. | X80695 | 4179 |
| GCCCGAGGAA | | | 4180 |
| GCGCAGACTT | | | 4181 |
| TGCCAGCGCC | | | 4182 |
| TTGTGGGGGG | | | 4183 |
| TGGGCGCCTT | Human uroporphyrinogen decarboxylase mRNA, complet | M14016 | 4184 |
| TCATTGTAAT | | | 4185 |
| TACTAAAAAA | | | 4186 |
| GTGGCGGGTG | | | 4187 |
| GTGGTGGCAG | | | 4188 |
| GCTGGTCTGA | | | 4189 |
| TGATAATTCA | | | 4190 |
| GCAAAGAAAA | Human breast tumor autoantigen mRNA, complete sequ | U24576 | 4191 |
| GAGAGCTACA | Human electron transfer flavoprotein alpha-subunit | J04058 | 4192 |
| ATTATCCTGG | | | 4193 |
| ATAAATTGGG | H.sapiens mRNA for H ⁺ -ATP synthase subunit b. | X60221 | 4194 |
| TTTCAGATTG | Human transcriptional coactivator PC4 mRNA, comple | U12979 | 4195 |
| TTCATTTGCC | | | 4196 |
| GTGGCACACA | Human cortex mRNA containing an Alu repetitive ele | X51524 | 4197 |
| CTGGGCAAAC | | | 4198 |
| TTTTACTGGG | | | 4199 |

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| TGGGCCTGGC | | | 4200 |
| TGCCTGTAAT | Human NTera2D1 cell line mRNA containing L1 retrop | U61090 | 4201 |
| TCTTGTAAC | | | 4202 |
| TCTGTAATCC | Human phenol-sulfating phenol sulfotransferase mRN | L19999 | 4203 |
| GGAATAAATT | Human mRNA for cytochrome c1. | X06994 | 4204 |
| AACGAGGAAT | | | 4205 |
| GACTCTCTGT | Human gamma-tubulin mRNA, complete cds. | M61764 | 4206 |
| ACATCGTAGG | | | 4207 |
| CTGGATGCCG | Human RD protein (RD) mRNA, complete cds. | L03411 | 4208 |
| CCCCCTGGGA | | | 4209 |
| CACCCCCAGG | Human Gps2 (GPS2) mRNA, complete cds. | U28963 | 4210 |
| ATGGGCTGGT | | | 4211 |
| AGGTCCCTGT | | | 4212 |
| AGAGCCCTAG | Homo sapiens COX17 mRNA, complete cds. | L77701 | 4213 |
| GCCACTACCC | | | 4214 |
| GATCTTCGTA | | | 4215 |
| TCCATCTGTT | Human mRNA for ryudocan core protein. | D13292 | 4216 |
| GTGGGGTGAC | | | 4217 |
| GGTTTGTGTG | | | 4218 |
| GGAGGCAGGT | | | 4219 |
| GCTGGAGCTA | Human dihydrolipoamide dehydrogenase mRNA, complet | J03620 | 4220 |
| GCCTCTTCCC | | | 4221 |
| TTTCTTAAAG | Human mRNA for KIAA0324 gene, partial cds. | AB0023 | 4222 |
| GCCAAAAAAA | H.sapiens (TL7) mRNA from LNCaP cell line. | X75687 | 4223 |
| GACTGCGTGC | Homo sapiens cell cycle progression 2 protein (CPR | AF0117 | 4224 |
| GACTCAGGGA | | | 4225 |
| CTGCCAAGTT | H.sapiens mRNA for zyxin 2. | X95735 | 4226 |
| ATATTTTCCT | | | 4227 |
| ACTAACTGTG | H.sapiens RbAp48 mRNA encoding retinoblastoma bind | X74262 | 4228 |
| ACCTGAAACC | | | 4229 |
| ACCGTATTCC | | | 4230 |
| GCCAAACGTA | | | 4231 |
| CGGTTACTGT | | | 4232 |
| CAGCGCGCCC | | | 4233 |

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| AATCTGCGCC | Human interferon-induced 17-kDa/15-kDa protein mRNA | M13755 | 4234 |
| GGGGACTGAA | Homo sapiens mRNA for low molecular mass ubiquinon | D50369 | 4235 |
| TTAAAAGCCT | H.sapiens ckshs1 mRNA for Cks1 protein homologue. | X54941 | 4236 |
| GGCTGGTCTG | | | 4237 |
| GACTCTGGTG | | | 4238 |
| TGTGGGTGCT | H.sapiens mRNA for E-cadherin. | Z13009 | 4239 |
| AACCCGGGAG | Human primary Alu transcript. | U67828 | 4240 |
| AGTGCAAGAC | | | 4241 |
| TCAGCCTTCT | | | 4242 |
| TTGGAGATCT | Human NADH:ubiquinone oxidoreductase MLRQ subunit | U94586 | 4243 |
| ACAACCTCAAT | Human HepG2 3' region cDNA, clone hmd4h10. | D16936 | 4244 |
| TTACCTCCTT | | | 4245 |
| GCAGGGCCTC | H.sapiens mRNA for MAT8 protein. | X93036 | 4246 |
| GGAAGGGAGG | | | 4247 |
| AAGATCCCCG | | | 4248 |
| TGGTGACAGT | | | 4249 |
| ACTGAGGTGC | Homo sapiens FGF-1 intracellular binding protein (| AF0101 | 4250 |
| GCTTTCTCAC | | | 4251 |
| GATGACCCCC | | | 4252 |
| GACCAGAAAA | Human COX VIa-L mRNA for cytochrome c oxidase live | X15341 | 4253 |
| CCATTGCACT | Human phosphatidylinositol 3-kinase homolog (ATM) | U26455 | 4254 |
| ATCGGGCCCCG | | | 4255 |
| CTGCTATACG | Human ribosomal L5 protein mRNA, partial cds. | U76609 | 4256 |
| ACCTCAGGAA | Human high density lipoprotein binding protein (HB | M64098 | 4257 |
| AATGCAGGCA | Human S-adenosylhomocysteine hydrolase (AHCY) mRNA | M61832 | 4258 |
| TGGGGAGAGG | | | 4259 |
| GGAACGTGA | Homo sapiens Tspan-1 mRNA, complete cds. | AF0548 | 4260 |
| GGAAAAGTGG | Human HepG2 3' region Mbol cDNA, clone hmd3e05m3. | D17206 | 4261 |
| ATCAGTGGCT | prosome beta-subunit=multicatalytic proteinase com | S71381 | 4262 |
| GTGCTGGAGA | Human SnRNP core protein Sm D2 mRNA, complete cds. | U15008 | 4263 |
| GGGAGCCCCCT | H.sapiens mRNA for arrestin (partial). | Z11501 | 4264 |
| GCAGTGCCAC | | | 4265 |

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| GGGCTGGGGT | Human cell surface heparin binding protein HIP mRNA | U49083 | 4266 |
| CGCCGCGGTG | | | 4267 |
| TAAGGAGCTG | H.sapiens mRNA for ribosomal protein S26. | X69654 | 4268 |
| ATTCTCCAGT | Human mRNA for ribosomal protein L17. | X52839 | 4269 |
| AAGGAGATGG | H.sapiens mRNA for ribosomal protein L31. | X69181 | 4270 |
| ATAATTCTTT | Homo sapiens (clone cori-1cl5) S29 ribosomal prote | L31610 | 4271 |
| TGCAGCGCCT | H.sapiens mRNA for uridine phosphorylase. | X90858 | 4272 |
| TCCCATTAAG | | | 4273 |
| GTGAAGGCAG | Human v-fos transformation effector protein (Fte-1 | M84711 | 4274 |
| CAATAAATGT | Homo sapiens ribosomal protein L37 mRNA, complete | L11567 | 4275 |
| TAGGTTGTCT | Homo sapiens (clone 04) translationally controlled | L13806 | 4276 |
| CACAAACGGT | Human ribosomal protein S27 mRNA, complete cds. | U57847 | 4277 |
| TACCATCAAT | Human glyceraldehyde-3-phosphate dehydrogenase (GA | M33197 | 4278 |
| TTGGTCCTCT | Homo sapiens ribosomal protein L41 mRNA, complete | AF0268 | 4279 |
| TTCATACACC | | | 4280 |
| TCCCTATTAA | | | 4281 |
| TGCACGTTTT | Human mRNA from chromosome 15 gene with homology t | K03002 | 4282 |
| CCTATTTACT | Human cytochrome c oxidase subunit IV (COX4) mRNA, | M34600 | 4283 |
| AGTATCTGGG | Homo sapiens Arp2/3 protein complex subunit p41-Ar | AF0060 | 4284 |
| TAGCTCTATG | Human Na,K-ATPase alpha-1 subunit mRNA, complete c | U16798 | 4285 |
| CTGTTGATTG | Human clone C4E 3.2 (CAC)n/(GTG)n repeat-containin | U00947 | 4286 |
| CCCGACGTGC | | | 4287 |
| GCATAGGCTG | P43=mitochondrial elongation factor homolog [human | S75463 | 4288 |
| TGTGATCAGA | | | 4289 |
| TAATAAAGGT | | | 4290 |
| CAATAAACTG | | | 4291 |
| GAAGTGTGTC | | | 4292 |
| CACTTGCCCT | branchio-oto-renal syndrome candidate gene {3' reg | S82655 | 4293 |

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| CCCCATCGTC | | | 4294 |
| ACAAACTGTG | | | 4295 |
| GACTCACTTT | Human secreted cyclophilin-like protein (SCYLP) mR | M63573 | 4296 |
| TGGAGTGGAG | Human guanylate kinase (GUK1) mRNA, complete cds. | L76200 | 4297 |
| GCATAATAGG | H.sapiens mRNA for large subunit of ribosomal prot | X89401 | 4298 |
| GAGGGCCGGT | | | 4299 |
| GCTGCTCCCT | | | 4300 |
| GAAGATGTGT | | | 4301 |
| TCTGTCAAGA | transcript ch21=oligomycin sensitivity conferral p | S77356 | 4302 |
| GTTGGTCTGT | | | 4303 |
| CTGCCGAGCT | Human cyclin-selective ubiquitin carrier protein m | U73379 | 4304 |
| AGATCGAGAC | | | 4305 |
| TGCTTCATCT | | | 4306 |
| ATGAAACCCC | Human small cytoplasmic Alu transcript. | U67806 | 4307 |
| GGAAGGGGGA | | | 4308 |
| CACAGAGTCC | Human alpha-2-macroglobulin receptor-associated pr | M63959 | 4309 |
| CCAGGGGAGA | H.sapiens p27 mRNA. | X67325 | 4310 |
| TGTGGGAAAT | Human mRNA for antileukoprotease (ALP) from cervix | X04470 | 4311 |
| TCCCTATAAG | | | 4312 |
| TAGACTAGCA | Human globin gene. | M69023 | 4313 |
| GTGTGTGGTG | Human clone 23856 unknown mRNA, partial cds. | AF0071 | 4314 |
| GCCCATCGTC | | | 4315 |
| TCCCGTACAT | | | 4316 |
| GTGCTCTGTA | | | 4317 |
| ATGAGCTATG | | | 4318 |
| CCCTGATTTT | Human translation repressor NAT1 mRNA, complete cd | U76111 | 4319 |
| CCCTATTAAG | | | 4320 |
| CCCAGACTCC | | | 4321 |
| CACCTTCCAG | Human melanoma antigen p15 mRNA, complete cds. | U19796 | 4322 |
| TTCTCTCAAC | | | 4323 |
| ATCACAGTGT | Human nuclear-encoded mitochondrial serine hydroxy | L11932 | 4324 |
| GTGGTGTGCA | | | 4325 |
| GGCTCCTCGA | Homo sapiens tapasin (NGS-17) mRNA, complete cds. | AF0297 | 4326 |

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| GTGCCTAGGG | | | 4327 |
| GAGAAACCCC | Human small cytoplasmic Alu transcript. | U67802 | 4328 |
| AGCTGGAGTC | | | 4329 |
| AAAGTCTAGA | Human bcl-1 mRNA, complete CDS. | M73554 | 4330 |
| GTAGGGGTAA | | | 4331 |
| GCGGGAGGGC | | | 4332 |
| GTTTTTCATT | | | 4333 |
| CCACAGGAGA | | | 4334 |
| CCCTGCCTTG | Human mRNA for neurite outgrowth-promoting protein | X55110 | 4335 |
| CCATTGAAAC | Homo sapiens mRNA for Laminin-5 beta3 chain, compl | D37766 | 4336 |
| TCCTCAAGAT | Human mRNA for human protein homologous to DROER p | D85758 | 4337 |
| TCCTATTAAG | | | 4338 |
| CAGGAACGGG | Homosapiens ERK activator kinase (MEK2) mRNA. | L11285 | 4339 |
| CAAGGATCTA | | | 4340 |
| ATGATGCGGT | cytoplasmic antiproteinase=38 kda intracellular se | S69272 | 4341 |
| GAGCGGGATG | Human mRNA for proteasome subunit Y, complete cds. | D29012 | 4342 |
| GGGTCAAAAG | | | 4343 |
| ACTTTGAATG | | | 4344 |
| GCCCGCCTTG | Homo sapiens (clone mf.18) RNA polymerase II mRNA, | L37127 | 4345 |
| CCCGCCTCTT | | | 4346 |
| GCTTTGATGA | Human epoxide hydrolase mRNA, complete cds. | J03518 | 4347 |
| CGGACTCACT | | | 4348 |
| GGAAGCACGG | Human antisecretory factor-1 mRNA, complete cds. | U24704 | 4349 |
| AGTCTGATGT | | | 4350 |
| TGGCTAGTGT | Human mRNA for proteasome subunit z, complete cds. | D38048 | 4351 |
| ACTCAGAAGA | | | 4352 |
| GCCAGGGCGG | | | 4353 |
| GAATTAACAT | Human 14-3-3 epsilon mRNA, complete cds. | U54778 | 4354 |
| TCTGCCTGGG | | | 4355 |
| GCTCTCTATG | H.sapiens mRNA translocon-associated protein delta | Z69043 | 4356 |
| CTGGGTCTCC | H.sapiens BBC1 mRNA. | X64707 | 4357 |
| GAAATGATGA | Human mRNA for c-myc binding protein, complete cds | D89667 | 4358 |
| TTAGCAATAA | | | 4359 |

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| GGAGCGTGGG | | | 4360 |
| TTCTGGCTGC | Human mRNA for core I protein, complete cds. | D26485 | 4361 |
| GTTCTCCCAC | | | 4362 |
| GTAATCCTGC | | | 4363 |
| GGAAAAA | Human (clone SF2) hepatocyte growth factor (HGF) m | M73240 | 4364 |
| TTTCAGGGGA | | | 4365 |
| TATCACTCTG | Homo sapiens male-enhanced antigen (Mea) mRNA, com | L10400 | 4366 |
| AGCTGTCCCC | | | 4367 |
| TTGGTCAGGC | Human melanoma antigen recognized by T-cells (MART | U06452 | 4368 |
| GCATATTAAA | Human mRNA for XP-C repair complementing protein (| D21090 | 4369 |
| CTGCTCATCC | Human aldehyde dehydrogenase ALDH7 mRNA, complete | U10868 | 4370 |
| GTGTAAATGG | | | 4371 |
| GGGGCCCCCA | Homo sapiens copper chaperone for superoxide dismu | AF0022 | 4372 |
| GGGAGGAGGG | | | 4373 |
| GGGACGAGTG | H.sapiens (TL27) mRNA from (PC3) cell line. | X75684 | 4374 |
| GGCCCTGGTG | Homo sapiens mRNA for HsGAK, complete cds. | D88435 | 4375 |
| TCTGCACATC | | | 4376 |
| GCTGGGGGAC | Human gamma-glutmyl transpeptidase-related protein | M64099 | 4377 |
| ATGGCCTGTA | | | 4378 |
| GCAGAGGCCT | | | 4379 |
| GAGTAGAGGC | H.sapiens mRNA for sphingomyelinase. | X59960 | 4380 |
| GAGGTGCTCT | | | 4381 |
| GAGGCCTCAG | | | 4382 |
| GACCAGCCTT | | | 4383 |
| AAATCCTAGA | | | 4384 |
| GGAGTAAGGG | | | 4385 |
| TGTGTCAAAG | | | 4386 |
| ACCTGCCCCCT | | | 4387 |
| AAAACAGTGG | | | 4388 |
| TTTTATGGAA | | | 4389 |
| TTTTACAGTA | | | 4390 |
| TTGTACAACA | | | 4391 |
| TTGCTAAAGG | | | 4392 |
| TCGTTGTTTA | | | 4393 |
| TTAGCTTGTT | | | 4394 |

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| CGGATCTGCT | | | 4395 |
| TGGTAGTTAC | | | 4396 |
| TGGGCTGGGG | | | 4397 |
| TGGCCCGACG | Human mRNA for 8-oxo-dGTPase, complete cds. | D16581 | 4398 |
| TGGATAATTC | | | 4399 |
| AATATTGTGG | | | 4400 |
| TGATGCTACC | | | 4401 |
| TTCCTCGGGC | | | 4402 |
| ACGACGGCCG | | | 4403 |
| CTTGGTGCTG | | | 4404 |
| AGCCGGGATG | LMP2=proteasome LMP2.s {alternatively spliced} [hu | S75169 | 4405 |
| AGATGCCCTT | | | 4406 |
| AGAGTCCTGC | | | 4407 |
| AGACCATATT | Homo sapiens sin3 associated polypeptide p18 (SAP1 | U96915 | 4408 |
| ACTTAAGGAA | | | 4409 |
| AGGCCATAGG | | | 4410 |
| ACTCAAAGAC | Human C/EBP gamma mRNA, complete cds. | U20240 | 4411 |
| AGGCCCCACG | | | 4412 |
| ACCTTTACTG | | | 4413 |
| ACCATTGGAT | H.sapiens mRNA for interferon- induced 17kDa membra | X84958 | 4414 |
| AAGTGGAAGC | | | 4415 |
| AACATAAATT | | | 4416 |
| AACAGACACA | | | 4417 |
| AAAGTGAAGA | | | 4418 |
| ACTCAGACCA | | | 4419 |
| CACCGGGTAG | Human mRNA for KIAA0221 gene, complete cds. | D86988 | 4420 |
| CGCCTTTACT | | | 4421 |
| CCTTTTGTG | | | 4422 |
| CCTCTTCAGG | | | 4423 |
| CCGCCCCCAG | Human islet cell autoantigen ICAp69 mRNA, complete | U38260 | 4424 |
| CCCCCCTGGA | | | 4425 |
| CCCCCAGTTG | | | 4426 |
| AGCTGGAAAG | | | 4427 |
| CACCTTAATT | | | 4428 |
| AACAAGGTGA | | | 4429 |
| CAATGTCTCA | | | 4430 |
| CAATGCTGCC | | | 4431 |
| ATTGTGAGGC | | | 4432 |
| ATAATTGACT | | | 4433 |

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| AGGTCTGCCA | chlordecone reductase homolog {clone HAKRc} [human | S68290 | 4434 |
| AGGCCTCGGC | | | 4435 |
| CAGTGGGGTT | | | 4436 |
| CCGGTTGGCA | | | 4437 |
| CCAGGCACGC | Homo sapiens XAP-5 mRNA, complete cds. | AD0015 | 4438 |
| CGTGTTGTTC | | | 4439 |
| CGTGGGGTGG | | | 4440 |
| CGCCAGGCGG | | | 4441 |
| CGACGCTTGA | | | 4442 |
| CGACCGTGCC | | | 4443 |
| CTTTGCTGTG | Human mRNA for KIAA0045 gene, complete cds. | D28476 | 4444 |
| CCGTCCCAAG | | | 4445 |
| GAAATTTAAA | Human mRNA for HMG-1, complete cds. | D63874 | 4446 |
| CCGAGCAACT | | | 4447 |
| CCCTGTAATA | | | 4448 |
| CCCTGGGCTT | | | 4449 |
| CCCGTCGTCC | | | 4450 |
| CCCCAGCCCA | | | 4451 |
| AAAACCTTAGA | Human mRNA for CD59, an LY-6-like protein regulati | X16447 | 4452 |
| CCTTTCACAC | Homo sapiens general transcription factor 2-I (GTF | AF0357 | 4453 |
| GATGGCTGGT | | | 4454 |
| GCTGGCTGTT | Human phosphatidylinositol (4,5)bisphosphate 5-pho | U45973 | 4455 |
| GCGGGCGCGG | Homo sapiens TTF-I interacting peptide 20 mRNA, pa | AF0005 | 4456 |
| GCGCTGGTAC | | | 4457 |
| GCGACGGCCG | | | 4458 |
| GCCTGGTGAC | Homo sapiens Fas-binding protein Daxx mRNA, comple | AF0159 | 4459 |
| GCCCTTCCTG | | | 4460 |
| CTTCCCACTG | | | 4461 |
| GCCACCAGAC | | | 4462 |
| CCAGGATATT | | | 4463 |
| GAGGTGGTGC | | | 4464 |
| GAGAGCCTGC | | | 4465 |
| GAGAAGCCCA | | | 4466 |
| GACGACTGAC | | | 4467 |
| GACATCCCGC | | | 4468 |
| GAAGTTATAA | Homo sapiens clone 23915 mRNA sequence. | AF0381 | 4469 |

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| GCCCCCTGAAG | | | 4470 |
| AATAGGGTCA | | | 4471 |
| CCCAAACGTG | | | 4472 |
| AGAAATGTAT | Human mRNA for transcription factor AREB6, complet | D15050 | 4473 |
| ACTGTGGCGG | | | 4474 |
| ACTGGAGTTT | Human poly(A) polymerase mRNA, 3' UTR. | AF0029 | 4475 |
| ACTGATCTGC | | | 4476 |
| ACTCTTCTAA | | | 4477 |
| AGATTTTCTC | Human fumarylacetoacetate hydrolase mRNA, complete | M55150 | 4478 |
| ACCCCCTTCC | | | 4479 |
| AGCATATCTT | | | 4480 |
| AATAAAGCAA | | | 4481 |
| AAGTTGGAGG | | | 4482 |
| AAGCGAATGC | | | 4483 |
| AAGATTGGGG | CD44=CD44SP {alternatively spliced} [human, breast | S66400 | 4484 |
| AACTCCCAGT | | | 4485 |
| AACCTCGAGT | | | 4486 |
| ACGCAGGCGC | Human nucleosome assembly protein 2 mRNA, complete | U77456 | 4487 |
| ATGTACTAAA | H.sapiens mRNA for TFG protein. | Y07968 | 4488 |
| CCACACAAGC | | | 4489 |
| CATAAAGTTT | | | 4490 |
| CAGGGAGCGC | Homo sapiens TPA inducible protein mRNA, complete | AF0561 | 4491 |
| CAGATGAGAT | | | 4492 |
| CACTGCCTTT | Homo sapiens fb19 mRNA. | Y13247 | 4493 |
| CACAGCGCCC | | | 4494 |
| AGACTTGGCA | Homo sapiens actin-related protein Arp3 (ARP3) mRN | AF0060 | 4495 |
| ATGTGGTTGT | Human replication factor C, 37-kDa subunit mRNA, c | M87339 | 4496 |
| TTTTATCTGG | H.sapiens mRNA for ITBA2 protein. | X92896 | 4497 |
| ATGGCGGGTG | | | 4498 |
| ATGCTAAAAA | | | 4499 |
| AGTAACTGAG | | | 4500 |
| AGCTGGTTTC | Homo sapiens Pig8 (PIG8) mRNA, complete cds. | AF0103 | 4501 |
| AGCTCGTACA | | | 4502 |
| AGCCACCGTG | | | 4503 |
| CAAAGGCTGT | | | 4504 |
| CACAGGCAAA | Human mRNA for KIAA0005 gene, complete cds. | D13630 | 4505 |

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| AGCCACTGTG | | | 4506 |
| GCAAAACCCT | Human clone 11 Alu repeat sequence. | U02053 | 4507 |
| GATTTGAGAA | | | 4508 |
| GATGGCTGCC | | | 4509 |
| GAGGTGCCGG | | | 4510 |
| GACAGTGACG | Human mRNA for zinc finger protein, complete cds. | D45213 | 4511 |
| GGGAAGGCAC | | | 4512 |
| CCCATCGCCC | | | 4513 |
| GGGACGGGTG | Human primary Alu transcript. | U67812 | 4514 |
| CAAATAAAAA | Homo sapiens (clone CD18) tumor necrosis factor re | L04270 | 4515 |
| ATTTGAGCAG | | | 4516 |
| ATGGCGATCT | | | 4517 |
| AGTGCCGTGT | Human p78 protein mRNA, complete cds. | M33882 | 4518 |
| AGGGTTGGAA | | | 4519 |
| AAACCTGGGA | | | 4520 |
| CTGCTTAAGG | | | 4521 |
| TTTCCAGTGG | Human WD repeat protein HAN11 mRNA, complete cds. | U94747 | 4522 |
| ATCTTGAACA | | | 4523 |
| AGTAGGAGGG | | | 4524 |
| AGGAAAAGAT | Human 1.1 kb mRNA upregulated in retinoic acid tre | U09196 | 4525 |
| AGCTATTCCT | Human multiple exostoses type II protein EXT2.1 mR | U72263 | 4526 |
| AAGGGCAGTG | | | 4527 |
| AACCAGAGGT | | | 4528 |
| GCCACGTGGA | Homo sapiens mRNA for villin-like protein, complet | D88154 | 4529 |
| TTTTTAATGT | Human H3.3 histone class C mRNA, complete cds. | M11353 | 4530 |
| ACCACAGGGG | | | 4531 |
| TGCTGCCTGT | Human mRNA for BST-2, complete cds. | D28137 | 4532 |
| TAAAGCTGTT | H.sapiens mRNA for E2 protein. | X53251 | 4533 |
| GTGTGGGGTG | | | 4534 |
| GTGGTGGGCA | MJD1=MJD1 protein {CAG repeats} [human, brain, mRN | S75313 | 4535 |
| GTGAAACCTG | Human Krit1 mRNA, complete cds. | U90268 | 4536 |
| GTAGCGCGCC | | | 4537 |
| AAAGGTTGGT | Human GT335 mRNA, complete cds. | U53003 | 4538 |
| CCAGCCTGGG | | | 4539 |
| AGGGCTACGG | | | 4540 |
| CTTTTGTGC | | | 4541 |

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| CTTCTGTGTA | Homo sapiens immunophilin homolog ARA9 mRNA, compl | U78521 | 4542 |
| CTCTTCAGGA | Homo sapiens phosphomevalonate kinase mRNA, comple | L77213 | 4543 |
| CTCTCAATGG | H.sapiens mRNA for GlcNac-1-P transferase. | Z82022 | 4544 |
| CCCAATTTTC | | | 4545 |
| GATGGAATGT | | | 4546 |
| CCATAATGTT | | | 4547 |
| GCAAAAAAAT | | | 4548 |
| CCACTGCATT | H.sapiens INE1 mRNA. | Y10696 | 4549 |
| CAGGCCTGGC | | | 4550 |
| CAATCACAAA | | | 4551 |
| CAAGAGCGAG | | | 4552 |
| ATGTTGCCCC | Homo sapiens HMG box containing protein 1 mRNA, co | AF0192 | 4553 |
| ATGTTAGGGA | Homo sapiens vesicle soluble NSF attachment protei | AF0358 | 4554 |
| CCCAAGGTGT | | | 4555 |
| TAAACTGTTT | | | 4556 |
| ACACTGCACT | | | 4557 |
| AAACTGTGGT | | | 4558 |
| AAACCTCTTC | | | 4559 |
| TTTCCAATCT | Homo sapiens vascular endothelial growth factor (V | AF0247 | 4560 |
| TTGAATTCTT | | | 4561 |
| TTACTTATAC | | | 4562 |
| GACATAAATC | Human mRNA for KIAA0113 gene, partial cds. | D30755 | 4563 |
| TACAAACCTG | | | 4564 |
| CACTTGAAAA | | | 4565 |
| GTGAGCAAGA | Human mRNA for a presumptive KDEL receptor. | X55885 | 4566 |
| GGGGCTGGGG | | | 4567 |
| GGGATTTGGC | | | 4568 |
| GGCACAGTAA | | | 4569 |
| GCTTTCTCAA | | | 4570 |
| GCTTTCATTG | | | 4571 |
| TGCACCACAG | | | 4572 |
| CCGAGTTTTT | | | 4573 |
| ATGCGGAGTC | | | 4574 |
| GCTGCCAGCT | | | 4575 |
| GCTAAAAAAA | | | 4576 |
| GATCTCATCT | | | 4577 |
| GAGACCTTGG | Human betaB3 crystallin mRNA, partial cds. | U71216 | 4578 |

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| GAAGATGCCT | Human mRNA for UDP-galactose translocator, complet | D84454 | 4579 |
| GGATCCTTGG | | | 4580 |
| CCTGTAGTTC | | | 4581 |
| GGGCTTTACC | | | 4582 |
| CCCTGGCAAT | | | 4583 |
| CCCAGATGAT | | | 4584 |
| CCAGATTTTG | Human mRNA for KIAA0253 gene, partial cds. | D87442 | 4585 |
| CCACTGCCCT | | | 4586 |
| CAGCCTGTCG | | | 4587 |
| CAGCCAGGGG | | | 4588 |
| CTGGGTGCCC | | | 4589 |
| TCCCCGTAAA | | | 4590 |
| GCTTAGAAGT | | | 4591 |
| TTGTCCAGGC | | | 4592 |
| TTGCAATGCA | | | 4593 |
| TTACACCTGT | H.sapiens mRNA for caltractin. | X72964 | 4594 |
| TGGATTTTGG | Human mRNA for A-raf-1 oncogene. | X04790 | 4595 |
| TGGAAGTGTG | | | 4596 |
| GGAGAAGATG | | | 4597 |
| TCTATAGAGT | | | 4598 |
| AGTTTGGGCT | | | 4599 |
| TATTTATGGA | H.sapiens RON mRNA for tyrosine kinase. | X70040 | 4600 |
| TATCCTGGCT | | | 4601 |
| TAATTTTGGA | | | 4602 |
| GTGTGAATGT | Human 150 kDa oxygen-regulated protein ORP150 mRNA | U65785 | 4603 |
| GGTGGTACAC | | | 4604 |
| GGTAGCAGGG | | | 4605 |
| TGAGGCAGGG | Human syntaxin 5 mRNA, complete cds. | U26648 | 4606 |
| CTGCCCCCAC | | | 4607 |
| GGGCCCTTCC | Homo sapiens clone 24684 mRNA sequence. | AF0550 | 4608 |
| GGGCCCTGGC | Human k6h6 mRNA for lambda-immunoglobulin light ch | X13080 | 4609 |
| GGCCAAACAG | | | 4610 |
| GGCATTTTAA | | | 4611 |
| GCGGCCATCC | | | 4612 |
| GCAATGCAAA | | | 4613 |
| CAGCAGTAGC | H.sapiens mRNA for 218kD Mi-2 protein. | X86691 | 4614 |
| GACTTCACTT | | | 4615 |
| TACTATTAAT | | | 4616 |

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| CTCAGCCTGA | Human HepG2 3' region Mbol cDNA, clone hmd2f10m3. | D17172 | 4617 |
| CGTGTCTAGCA | Homo sapiens brain and reproductive organ-expresses | L38616 | 4618 |
| CCTTAGCTGG | | | 4619 |
| CCTGGAGCAA | | | 4620 |
| CCCCTGGATC | | | 4621 |
| AAACATTGGG | Human HepG2 3' region Mbol cDNA, clone hmd4f06m3. | D17237 | 4622 |
| GAGTCAGGAG | | | 4623 |
| TTCTCACCAC | Human myosin light chain 1 slow a (MLC1sa) mRNA, c | M31211 | 4624 |
| ATTACAAACC | | | 4625 |
| ACTGCTCATT | | | 4626 |
| ACATCCCAGA | H.sapiens polyA site DNA. | Z24726 | 4627 |
| ACAAGGTGCG | | | 4628 |
| ACAAAAA | | | 4629 |
| AATTCAATTA | | | 4630 |
| TACACTGCTT | | | 4631 |
| TTTCTGCTCC | | | 4632 |
| TACCCTAGAA | Human estrogen receptor-related protein (variant E) | M69297 | 4633 |
| TGGGCCCCAC | | | 4634 |
| TGCTGCCTCA | Homo sapiens hook2 protein (HOOK2) mRNA, complete | AF0449 | 4635 |
| TCTTTCCCCA | | | 4636 |
| TCAGGGAGAT | | | 4637 |
| TATGTATGTT | | | 4638 |
| TATCCATACC | Human mRNA for hydrogen carrier protein, a compone | D00723 | 4639 |
| ATCTCTATCC | | | 4640 |
| TTTGGAATC | | | 4641 |
| GATTCCGTGA | | | 4642 |
| GCAATCCACA | | | 4643 |
| GCAACTCGTT | | | 4644 |
| GCAACACCCC | | | 4645 |
| GCAAAACCGT | | | 4646 |
| GATTTGGAGA | | | 4647 |
| GATTTCAGCT | | | 4648 |
| GATTGTGCAA | Human mRNA for KIAA0183 gene, partial cds. | D80005 | 4649 |
| GCCCCCTGGA | | | 4650 |
| GATTGCTGGA | Human dihydropteridine reductase (hDHPR) mRNA, com | M16447 | 4651 |
| GCACCACTGC | | | 4652 |
| GATTCAATAA | | | 4653 |

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| GATTAGCACC | | | 4654 |
| GATTACCTGT | | | 4655 |
| GATGTTGGGG | | | 4656 |
| GATGTGAAAT | | | 4657 |
| GATGTCATCA | H.sapiens XG mRNA (clone R4(607)). | Z48515 | 4658 |
| GATGGCCAGG | | | 4659 |
| GATTGGCTGG | | | 4660 |
| GCATCTGTTT | | | 4661 |
| CATTTTCAAG | | | 4662 |
| GCCCCCCCAC | | | 4663 |
| GCCCACTGTA | | | 4664 |
| GCCACTGCAC | | | 4665 |
| GCCAAGGGGT | ArgRS=arginyl-tRNA synthetase (human, ataxia-telan | S80343 | 4666 |
| GCCAAATTAG | | | 4667 |
| GCATTGTGGT | | | 4668 |
| GCAATGAGGT | Human mRNA for KIAA0176 gene, partial cds. | D79998 | 4669 |
| GCATCTTCAA | Human lymphocyte dihydropyrimidine dehydrogenase m | U20938 | 4670 |
| GCACAGAGCC | | | 4671 |
| GCATCAAGTT | | | 4672 |
| GCAGTCGCCA | | | 4673 |
| GCAGCTCGCT | | | 4674 |
| GCAGCGCGCC | Human G protein-coupled receptor mRNA, complete cd | U35398 | 4675 |
| GCAGCCCTAC | | | 4676 |
| GCACTTACCA | | | 4677 |
| GCACCCAAGG | | | 4678 |
| GATCTGTTCC | | | 4679 |
| GCATTGTGAC | | | 4680 |
| GACTGGAAAG | | | 4681 |
| GATGGAGAAT | | | 4682 |
| GAGAGTAACA | | | 4683 |
| GAGAAGTCAG | | | 4684 |
| GAGAAGCGGC | | | 4685 |
| GAGAAGAAGG | | | 4686 |
| GACTTTGGAG | | | 4687 |
| GACTTACCTG | | | 4688 |
| GAGGAAAGCT | | | 4689 |
| GACTGGAAGG | | | 4690 |
| GAGGAAATGG | | | 4691 |
| GACTCTGGGG | | | 4692 |
| GACTACCTTT | | | 4693 |
| GACGACCACG | | | 4694 |
| GACCTGTATG | | | 4695 |

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| GACCTGCCCCG | | | 4696 |
| GACCTCCAAG | | | 4697 |
| GACAGGTAAC | | | 4698 |
| GACAGGTAAA | | | 4699 |
| GACTGTTGCT | | | 4700 |
| GAGGTGGATG | | | 4701 |
| GCCCGTCAGG | | | 4702 |
| GATCTCGCTT | | | 4703 |
| GATCTAGAAA | | | 4704 |
| GATCGCACGT | | | 4705 |
| GATCCTGGAT | | | 4706 |
| GATCCCAAAT | | | 4707 |
| GATCAATGGA | Human mRNA for KIAA0060 gene, complete cds. | D31766 | 4708 |
| GAGATGCTGC | | | 4709 |
| GAGTGAGCCT | | | 4710 |
| GATGAGTGGA | Human ferredoxin mRNA, complete cds. | M34788 | 4711 |
| GAGGGCCTGA | | | 4712 |
| GAGGGAAAAA | | | 4713 |
| GAGGCTGAGG | | | 4714 |
| GAGGCGGCTG | | | 4715 |
| GAGGCCCTGC | | | 4716 |
| GAGGCCAAAG | | | 4717 |
| GAGGAATTTG | | | 4718 |
| GAGGAAGACG | | | 4719 |
| GATAAATATT | | | 4720 |
| GGAGAGGAAG | | | 4721 |
| GGATCTGGCC | | | 4722 |
| GGATCCCCAA | | | 4723 |
| GGAGTAATAA | Human Fc-gamma RIII-1 cDNA for Fc- gamma receptor I | X16863 | 4724 |
| GGAGGTGCTC | | | 4725 |
| GGAGGGGTGT | | | 4726 |
| GGAGGCAGAA | | | 4727 |
| GGAGCCTTGG | | | 4728 |
| GCCCCCCCCC | | | 4729 |
| GGAGCCAGCT | | | 4730 |
| GGATTTGGCT | | | 4731 |
| GGA CTCTGGT | | | 4732 |
| GGA CT CATCC | | | 4733 |
| GGACACATCC | | | 4734 |
| GGACAAGATA | | | 4735 |
| GGAAGTGTGT | | | 4736 |
| GGAAGGCAAG | | | 4737 |
| GGAACCTGGG | | | 4738 |

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| GGAGCCTTCC | | | 4739 |
| GGCCAGGGCG | | | 4740 |
| GGCCTGTATG | | | 4741 |
| GGCCTGGAAT | | | 4742 |
| GGCCTGCTGG | | | 4743 |
| GGCCGTGTGA | | | 4744 |
| GGCCCTGGAC | H.sapiens mRNA for galectin-8. | X91790 | 4745 |
| GGCCCGTCAC | | | 4746 |
| GGCCCGAGTT | | | 4747 |
| GGATGGGTGT | | | 4748 |
| GGCCAGGTAA | | | 4749 |
| GGATTAGGGT | | | 4750 |
| GGCATCATCA | | | 4751 |
| GGCAGGACAC | | | 4752 |
| GGCAGCTATA | | | 4753 |
| GGCAGCAGTA | | | 4754 |
| GGCACGTTTT | | | 4755 |
| GGCAAAACCC | | | 4756 |
| GGATTTTGGC | | | 4757 |
| GCTTCTCTAA | | | 4758 |
| GGCCCATATG | | | 4759 |
| GCCTCCCAGG | | | 4760 |
| GCTTTTtagg | | | 4761 |
| GCGACTCGAT | | | 4762 |
| GCGACGGCAG | | | 4763 |
| GCGAACGTGG | | | 4764 |
| GCCTTGTTCA | | | 4765 |
| GCCTTGCCTG | Human mRNA for KIAA0280 gene, partial cds. | D87470 | 4766 |
| GCCTTCCGTG | | | 4767 |
| GCGCCTGCCG | | | 4768 |
| GCCTGCGCTG | | | 4769 |
| GCGCGCCGCT | | | 4770 |
| GCCTCCAGAT | | | 4771 |
| GCCTCCACAA | | | 4772 |
| GCCTCAGCGC | | | 4773 |
| GCCGGTTGGC | | | 4774 |
| GCCGGGGAAG | | | 4775 |
| GCCGGAGGGC | | | 4776 |
| GCCGAGGGAG | | | 4777 |
| GCCCTGATTT | Human interferon regulatory factor 5 (Humirf5) mRN | U51127 | 4778 |
| GCCTGTGGAT | | | 4779 |
| GCTCTCATCC | | | 4780 |
| GACACCAGCC | | | 4781 |
| GCTTCAGTGG | | | 4782 |

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| GCTGGGTAA | | | 4783 |
| GCTGGGAGTC | | | 4784 |
| GCTGGGACTA | | | 4785 |
| GCTGACTTGC | | | 4786 |
| GCTGACACTG | | | 4787 |
| GCGCCCAGCC | | | 4788 |
| GCTCTGCCCC | | | 4789 |
| GCTTCTGGCA | | | 4790 |
| GCTCGTGGTC | | | 4791 |
| GCTCAAAAAA | | | 4792 |
| GCTAAAGGTT | | | 4793 |
| GCTAAACTGG | | | 4794 |
| GCGGTTACTG | | | 4795 |
| GCGGCCGCCG | | | 4796 |
| GCGGCAGTCC | | | 4797 |
| GCGCGTGCTG | | | 4798 |
| GCTCTGTTCA | Homo sapiens Ser/Arg-related nuclear matrix protei | AF0489 | 4799 |
| CCCTGCCCTT | | | 4800 |
| CCTAACTGAC | | | 4801 |
| CCGTCCGGTG | | | 4802 |
| CCGTCCAAAG | | | 4803 |
| CCGGTTGATG | | | 4804 |
| CCGGGTTATT | | | 4805 |
| CCGCTACGGA | | | 4806 |
| CCGAGTGCTC | | | 4807 |
| GACAGGCTGG | Human collagen type XVIII alpha 1 (COL18A1) mRNA, | L22548 | 4808 |
| CCCTGGGGTC | | | 4809 |
| CCTCATAAGG | | | 4810 |
| CCCTGCCCTC | | | 4811 |
| CCCTCTTTGT | Homo sapiens MutS homolog (MSH5) mRNA, complete cd | AF0347 | 4812 |
| CCCTCTGGAT | | | 4813 |
| CCCTCCTGCT | | | 4814 |
| CCCTCCCAGC | | | 4815 |
| CCCTCAGCAC | Human mRNA for vascular anticoagulant-beta (VAC-be | X16662 | 4816 |
| CCCTCACAGA | | | 4817 |
| CCCTTTGAAC | | | 4818 |
| CCTGGCCCTT | | | 4819 |
| CCTTGGAGAA | | | 4820 |
| CCTTCTGGTG | Human protein tyrosine kinase mRNA, complete cds. | U02680 | 4821 |
| CCTTCCTCAT | | | 4822 |
| CCTTATATTT | Human mRNA for TPRD, complete | D83077 | 4823 |

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| | cds. | | |
| CCTGTTGTCC | | | 4824 |
| CCTGTATCCC | | | 4825 |
| CCTGTAATCA | | | 4826 |
| CCTAGCAGAG | | | 4827 |
| CCTGTAAACC | | | 4828 |
| CCTATCGTCC | | | 4829 |
| CCTGGCCCTC | | | 4830 |
| CCTGCCCCCT | | | 4831 |
| CCTGAGAATT | | | 4832 |
| CCTCCCCTGC | | | 4833 |
| CCTCCAGTAC | | | 4834 |
| CCTCCAGCCA | | | 4835 |
| CCTCCAGCAG | | | 4836 |
| CCCGAGGAAG | | | 4837 |
| CCTGTAAAGC | | | 4838 |
| CCAATGCACT | | | 4839 |
| CCCTAGGAGA | | | 4840 |
| CCAGAGTCTC | | | 4841 |
| CCACTTGCCC | | | 4842 |
| CCACTTCCTC | | | 4843 |
| CCACTGTTTC | | | 4844 |
| CCACTGCACG | | | 4845 |
| CCACTCAATA | | | 4846 |
| CCAGGCCCTT | | | 4847 |
| CCACCTCCCA | | | 4848 |
| CCAGTGTCTG | | | 4849 |
| CCAATGAACT | | | 4850 |
| CCAATAAAAG | | | 4851 |
| CCAAGGGCTT | | | 4852 |
| CCAACTCTCA | | | 4853 |
| CCAACCCTGG | | | 4854 |
| CCAAAGCCAG | | | 4855 |
| CCAAAGAGTA | | | 4856 |
| ATGGCCCATA | H.sapiens mRNA for putative carboxylesterase. | Y09616 | 4857 |
| CCACGTGTCC | | | 4858 |
| CCCATCGGTC | | | 4859 |
| CGAAGAGCCA | | | 4860 |
| CCCCTAATTG | | | 4861 |
| CCCCGGCCAG | | | 4862 |
| CCCCCTGCAA | | | 4863 |
| CCCCCCACAC | | | 4864 |
| CCCCCAGCCC | | | 4865 |
| CCCCATACTA | Human mRNA for KIAA0279 gene, partial cds. | D87469 | 4866 |

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|-------------|--|--------|------|
| CCAGCGCACC | | | 4867 |
| CCCATCGTGG | | | 4868 |
| CCCGCCTGGC | | | 4869 |
| CCCAGGAGCA | | | 4870 |
| CCCAGCTGGA | | | 4871 |
| CCCAGCCTCT | | | 4872 |
| CCCACCGGTG | | | 4873 |
| CCCAAGTGTC | | | 4874 |
| CCATTGCTCT | | | 4875 |
| CCATCTTGGA | | | 4876 |
| CCATATGATC | | | 4877 |
| CCCATTGTC | | | 4878 |
| CTTATTGTCC | | | 4879 |
| CTGGGAGCCC | | | 4880 |
| CTTTCCCAGC | | | 4881 |
| CTTTCCAGAC | | | 4882 |
| CTTTATGTGT | Human (ard-1) mRNA, complete cds. | U14575 | 4883 |
| CTTGTGGTAC | | | 4884 |
| CTTGGTAATT | | | 4885 |
| CTTGCGTGAG | | | 4886 |
| CTTTCTCTAA | | | 4887 |
| CTTCCTGCTC | | | 4888 |
| CTTTTAAGAA | | | 4889 |
| CTTATTGCCC | | | 4890 |
| CTTATGGTCC | | | 4891 |
| CTGTTTGGTG | | | 4892 |
| CTGTGTGCCA | | | 4893 |
| CTGTAGCAGT | | | 4894 |
| CTGGTGAGTG | | | 4895 |
| CTGGGTTAAC | | | 4896 |
| CCTTTCTCCT | | | 4897 |
| CTTCCTGTGA | | | 4898 |
| GAAGCAGCAG | | | 4899 |
| GGCGCACTCT | | | 4900 |
| GACAAGTTGG | | | 4901 |
| GAATCCTGTG | | | 4902 |
| GAATACAGTT | | | 4903 |
| GAAGTTCTCT | H.sapiens mRNA for 21-Glutamic Acid-Rich Protein (| X93498 | 4904 |
| GAAGGGATTT | | | 4905 |
| GAAGGATGTG | | | 4906 |
| CTTTCCTGTT | | | 4907 |
| GAAGCAGGGC | | | 4908 |
| CTGGGAACAT | | | 4909 |
| GAACCTCTGAC | | | 4910 |
| GAACGCTGGG | | | 4911 |

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| GAACGACACG | | | 4912 |
| GAACCTTCAG | | | 4913 |
| GAACACCTCC | | | 4914 |
| GAAAGTCGGA | | | 4915 |
| GAAAATATAC | | | 4916 |
| GAAAAGGGCA | | | 4917 |
| GAAGCATCCC | | | 4918 |
| CGGCGATCAT | | | 4919 |
| CTGGGTAA | | | 4920 |
| CTAGGTTAAT | | | 4921 |
| CTAGCAGCTT | | | 4922 |
| CTACAGACTT | | | 4923 |
| CTAAGATTTC | | | 4924 |
| CTAAGACCTT | | | 4925 |
| CTAAAATGCT | Human glycogenin mRNA, complete cds. | U31525 | 4926 |
| CTATGGTAAT | | | 4927 |
| CGGGTCCTCT | | | 4928 |
| CTATGTGTTA | Human RNA helicase A mRNA, complete cds. | L13848 | 4929 |
| CGGACAAACC | | | 4930 |
| CGCCTGTTAG | | | 4931 |
| CGCCTGGGGT | | | 4932 |
| CGCCGCCCGG | | | 4933 |
| CGCCCTCAAA | | | 4934 |
| CGAGTCAACA | Homo sapiens Na ⁺ /H ⁺ exchanger regulatory factor 2 | AF0357 | 4935 |
| CGAGACGCAT | | | 4936 |
| GACACCCCT | | | 4937 |
| CGGTTAAGAA | | | 4938 |
| CTGAATGAGA | | | 4939 |
| CTGGCTCCAT | | | 4940 |
| CTGGCTCATA | | | 4941 |
| CTGCTTGGGC | | | 4942 |
| CTGCTGCACT | | | 4943 |
| CTGCTCCAAA | | | 4944 |
| CTGCCCCACA | Human nuclear protein Skip mRNA, complete cds. | U51432 | 4945 |
| CTGCAGTGCG | | | 4946 |
| CTATAGTTTG | | | 4947 |
| CTGACATTTC | | | 4948 |
| CCTTTT | | | 4949 |
| CTGAAACCCC | | | 4950 |
| CTCTCTGTCC | | | 4951 |
| CTCGTCTGTG | | | 4952 |
| CTCCTCAAGC | | | 4953 |

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|--------------|---|--------|------|
| CTCCTCAACT | | | 4954 |
| CTCCTAATTG | | | 4955 |
| CTCCACCCGA | Human secretory protein (P1.B) mRNA, complete cds. | L15203 | 4956 |
| CTCAATGGCA | | | 4957 |
| CTGATTTGTA | Homo sapiens poly(ADP-ribose) glycohydrolase (hPAR | AF0050 | 4958 |
| TGATGCTCTT | | | 4959 |
| TGCCCTTAGG | | | 4960 |
| TGCCCTCGAA | | | 4961 |
| TGCCACTTTT | | | 4962 |
| TGCCACCAAC | | | 4963 |
| TGCATCTTCA | | | 4964 |
| TGCAGCGCTG | | | 4965 |
| TGCACGTTTC | | | 4966 |
| TCAGAGTAGG | | | 4967 |
| TGATGTTCCA | Human mRNA for KIAA0314 gene, partial cds. | AB0023 | 4968 |
| TGCTCCTACC | Human mRNA for IgG Fc binding protein, complete cd | D84239 | 4969 |
| TGATGATGTT | | | 4970 |
| TGATCAAAAA | | | 4971 |
| TGATATGTCA | | | 4972 |
| TGAGCTTGAT | | | 4973 |
| TGAGAAGAAG | | | 4974 |
| TGACTTATTA | | | 4975 |
| TGACCTGAAA | | | 4976 |
| TGATTTTGA | | | 4977 |
| TGGAGGTGGA | | | 4978 |
| TGGGTGTGTA | | | 4979 |
| TGGGTCATTT | | | 4980 |
| TGGGGGCCGA | | | 4981 |
| TGGGCTCTGA | Human mRNA for lysosomal sialoglycoprotein, comple | D12676 | 4982 |
| TGGGAGAAGT | | | 4983 |
| TGGCCCCAGG | Human mRNA for precursor of apolipoprotein CI (apo | X00570 | 4984 |
| TGGATGTACA | | | 4985 |
| TGCCTCAAAA | | | 4986 |
| TGGATATCAG | | | 4987 |
| TGCGTGACAG | | | 4988 |
| TGGAGAGCCT | | | 4989 |
| TGGAAGGGCC | | | 4990 |
| TGGAAGTGTGTA | | | 4991 |
| TGCTTTTGGG | | | 4992 |
| TGCTTTCTTT | | | 4993 |

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| TGCTTGTGTA | | | 4994 |
| TGCTGGAGAA | | | 4995 |
| TGAATGAATG | | | 4996 |
| TGGATCAGAT | | | 4997 |
| TCCCCGTGGC | Human mRNA for KIAA0018 gene, complete cds. | D13643 | 4998 |
| TGACCAGGCC | | | 4999 |
| TCCTAGGGTG | | | 5000 |
| TCCCTCAAGA | | | 5001 |
| TCCCTATTTA | | | 5002 |
| TCCCTATCAA | | | 5003 |
| TCCCTAATTA | | | 5004 |
| TCCCTAAAGC | | | 5005 |
| TCGCGGCCTG | | | 5006 |
| TCCCCTCAGG | | | 5007 |
| TCGGATGAAG | | | 5008 |
| TCCCAGTACA | | | 5009 |
| TCCACTGACG | | | 5010 |
| TCCACAAGCA | | | 5011 |
| TCATTTGCTC | | | 5012 |
| TCATCTGTGA | | | 5013 |
| TCATCTACAA | | | 5014 |
| TCATCGACAG | | | 5015 |
| GGCGACAGAG | | | 5016 |
| TCCCGCCCCC | | | 5017 |
| TCTGCGGGTG | | | 5018 |
| TGGTTTTGAG | | | 5019 |
| TGAAGCCTTG | | | 5020 |
| TGAAGCCAGT | | | 5021 |
| TGAAATACTG | | | 5022 |
| TGAAACTGCA | | | 5023 |
| TGAAAATTCA | | | 5024 |
| TCTTGGCCTT | | | 5025 |
| TCGATGATTA | | | 5026 |
| TCTGTAGCTT | | | 5027 |
| TGACACGTTT | | | 5028 |
| TCTGCCTCAA | | | 5029 |
| TCTGACAAAG | | | 5030 |
| TCTCTTGCTG | | | 5031 |
| TCTCTGAGCT | | | 5032 |
| TCTCTGAAAA | | | 5033 |
| TCTAAGTACG | | | 5034 |
| TCTAAGGAGT | | | 5035 |
| TCTAAAGGTC | | | 5036 |
| TCTGTTTTAG | | | 5037 |
| TTGGCCTTTT | | | 5038 |

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| TTCTGGGGGC | | | 5039 |
| TTGTATAGAC | Human DNA-binding protein (mbp-1) mRNA, complete c | M32019 | 5040 |
| TTGTAGTTTG | Homo sapiens putative seven pass transmembrane pro | AF0278 | 5041 |
| TTGTAAATGC | | | 5042 |
| TTGGTCCTTC | | | 5043 |
| TTGGTAAGAC | | | 5044 |
| TTGGGGACGG | | | 5045 |
| TTGTGGGTGC | | | 5046 |
| TTGGCTGGGC | | | 5047 |
| TTGTGTGATG | Human mRNA for KIAA0071 gene, partial cds. | D31888 | 5048 |
| TTGGCCGGGC | | | 5049 |
| TTGGCCACG | | | 5050 |
| TTGGACATTT | | | 5051 |
| TTGCTGTAGA | | | 5052 |
| TTGCTATTTA | | | 5053 |
| TTGCCACGG | | | 5054 |
| TTGAATTGAA | Homo sapiens mRNA for BCL7B protein, short isoform | AJ2239 | 5055 |
| TGGTAGACAT | | | 5056 |
| TTGGGGAAAA | | | 5057 |
| TTTGGAAAAA | | | 5058 |
| TTTTTTGAAA | Homo sapiens phospholipid scramblase mRNA, complet | AF0084 | 5059 |
| TTTTGTCTTA | | | 5060 |
| TTTTGTACGC | Human myleoid differentiation primary response pro | U70451 | 5061 |
| TTTTCTGTAC | | | 5062 |
| TTTTCACCAA | | | 5063 |
| TTTTATAAGG | Homo sapiens clk2 mRNA, complete cds. | L29218 | 5064 |
| TTTTAAAATA | | | 5065 |
| TTGTGATGTA | | | 5066 |
| TTTGTAATCG | | | 5067 |
| TTCTCTTCTT | | | 5068 |
| TTTGAGTGAC | | | 5069 |
| TTTGAGACTC | | | 5070 |
| TTTCCCTCCC | | | 5071 |
| TTTCCCAGGC | | | 5072 |
| TTTCATACAC | | | 5073 |
| TTTATTTAGT | | | 5074 |
| TTTATGAAGT | | | 5075 |
| TTTATCCCTT | | | 5076 |
| TTTGTTGAGA | | | 5077 |

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| TGTGCACAAT | | | 5078 |
| TTCTGTGAAT | Homo sapiens mRNA for caldesmon, 3' UTR. | AJ2238 | 5079 |
| TGTGTAAATC | Human mRNA for KIAA0121 gene, complete cds. | D50911 | 5080 |
| TGTGGTGGCG | | | 5081 |
| TGTGGGCCTC | | | 5082 |
| TGTGGGAGTA | | | 5083 |
| TGTGGCCTCA | | | 5084 |
| TGTGGAGCTG | | | 5085 |
| TGTGTGTGTG | Homo sapiens clone 23559 mRNA sequence. | AF0353 | 5086 |
| TGTGCCACTA | | | 5087 |
| TGTTACTTGC | | | 5088 |
| TGTGAATAAA | Human HepG2 3' region Mbol cDNA, clone hmd6c04m3. | D17286 | 5089 |
| TGTCTGGGCA | | | 5090 |
| TGTCGTGGAG | | | 5091 |
| TGTATTTTCC | | | 5092 |
| TGTATTTGTA | | | 5093 |
| TGTAATATGG | | | 5094 |
| TGTAAACTTG | | | 5095 |
| TCACCCACACA | | | 5096 |
| TGTGCCCCTG | | | 5097 |
| TTCAATACAC | | | 5098 |
| TTCTCAGCCC | | | 5099 |
| TTCTAATGTA | | | 5100 |
| TTCTAACTCC | | | 5101 |
| TTCTCTCCG | | | 5102 |
| TTCCGGAACT | | | 5103 |
| TTCCCTCTCC | | | 5104 |
| TTCCCAGACC | | | 5105 |
| TGTGTACCTG | | | 5106 |
| TTCACAGAGC | Homo sapiens mRNA for repressor protein, partial c | D30612 | 5107 |
| TGGTGACATT | Human fetal brain oculocerebrorenal syndrome (OCRL | U57627 | 5108 |
| TTCAAAAAAA | | | 5109 |
| TTAGTCCTCT | | | 5110 |
| TTACAGACTT | | | 5111 |
| TTAATTTTCA | | | 5112 |
| TTAAAACGTG | | | 5113 |
| TGTTTTGAGA | | | 5114 |
| TGTTCAAAGT | | | 5115 |
| TGTTATTACT | | | 5116 |
| TTCCACCTTC | | | 5117 |

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|-------------|---|--------|------|
| GTGATACACA | | | 5118 |
| GTGGACAGTA | Human mRNA for KIAA0100 gene, complete cds. | D43947 | 5119 |
| GTGCTTGTAC | Homo sapiens mRNA for glia maturation factor, comp | AB0011 | 5120 |
| GTGCGGAGGG | | | 5121 |
| GTGCGGAGGC | | | 5122 |
| GTGCCC GGCA | | | 5123 |
| GTGCCCACGG | | | 5124 |
| GTGCCAGGGA | | | 5125 |
| TCATACACCT | | | 5126 |
| GTGATGCCTG | | | 5127 |
| GTGGATT CAT | | | 5128 |
| GTGAGACCTT | | | 5129 |
| GTGACCCACG | | | 5130 |
| GTCATTTAGT | | | 5131 |
| GTATTTCCGG | | | 5132 |
| GTATCTGAGC | | | 5133 |
| GTATAATT TG | | | 5134 |
| G TAGGCACGG | | | 5135 |
| GTGATGGGGG | | | 5136 |
| GTGGCGAGTG | | | 5137 |
| GTGGTGCGCA | | | 5138 |
| GTGGGTACAA | | | 5139 |
| GTGGGGCCCC | | | 5140 |
| GTGGGCTAGG | | | 5141 |
| GTGGGCGGGC | | | 5142 |
| GTGGGCCAAG | | | 5143 |
| GTGGCGTGGT | | | 5144 |
| GTGGACCACG | | | 5145 |
| GTGGCGCGCG | | | 5146 |
| GTGGATGCTG | | | 5147 |
| GTGGCCCAGC | | | 5148 |
| GTGGCCACGC | | | 5149 |
| GTGGCCACCG | | | 5150 |
| GTGGCCAACG | | | 5151 |
| GTGGCACTTG | | | 5152 |
| GTGGCACTCT | | | 5153 |
| GTGGCACCAG | Human signal transducer and activator of transcrip | U47686 | 5154 |
| GTAATACTGA | | | 5155 |
| GTGGCGGAGG | | | 5156 |
| GGGAAAAGTG | Human Fas-associated death domain protein interleu | U86214 | 5157 |
| G TAGAAAAA | | | 5158 |
| GGGCATCTCC | | | 5159 |

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| GGGCAGCAAG | | | 5160 |
| GGGATTTGGG | | | 5161 |
| GGGATGCACA | | | 5162 |
| GGGAGCCCCC | | | 5163 |
| GGGACAAACA | | | 5164 |
| GGGCTGAACA | Homo sapiens U4/U6 small nuclear ribonucleoprotein | AF0163 | 5165 |
| GGGAAATCGC | | | 5166 |
| GGGCTGGGCT | | | 5167 |
| GGCTTTTAAG | | | 5168 |
| GGCTGTAGAG | | | 5169 |
| GGCTGGAGCT | | | 5170 |
| GGCTGCACGG | | | 5171 |
| GGCTGACCCT | | | 5172 |
| GGCTCATCTT | | | 5173 |
| GGCTAAGGAG | | | 5174 |
| CATTTATCAA | | | 5175 |
| GGGAAGAAAA | | | 5176 |
| GGGTGAGGGG | | | 5177 |
| GTGGTTCACA | | | 5178 |
| GGTTTTGTT | | | 5179 |
| GGTTTTGCTT | | | 5180 |
| GGTGGTGATG | Human (p23) mRNA, complete cds. | L24804 | 5181 |
| GGTGAGCGTG | H.sapiens HEK2 mRNA for protein tyrosine kinase re | X75208 | 5182 |
| GGTGACAATA | Homo sapiens mRNA for NKG2-CII activating NK recep | Y13055 | 5183 |
| GGTATCTGGG | | | 5184 |
| GGGCCAGCCC | | | 5185 |
| GGGTGGGCAG | | | 5186 |
| GTACGCATTC | S300-II=transcription factor [human, mRNA Partial, | S44184 | 5187 |
| GGGTGAAGGG | | | 5188 |
| GGGGTCCTTC | Human mRNA for KIAA0082 gene, partial cds. | D43949 | 5189 |
| GGGGGCCCCA | | | 5190 |
| GGGGCTGGAG | | | 5191 |
| GGGGCCAGGA | | | 5192 |
| GGGGAGGTAG | | | 5193 |
| GGGGAGAAGC | | | 5194 |
| GGGGAAGCAG | | | 5195 |
| GGGTTTGGCC | | | 5196 |
| TACCCTGGAA | Human class II alcohol dehydrogenase (ADH4) pi su | M15943 | 5197 |
| TAATCATTCA | | | 5198 |
| TAGCTGCCTT | | | 5199 |

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|-------------|---|--------|------|
| TAGCTATCCA | | | 5200 |
| TAGCCTTGGA | | | 5201 |
| TAGATCAGAG | | | 5202 |
| TAGAGAATGA | Human mRNA for TI-227H. | D50525 | 5203 |
| TACTTTATTT | | | 5204 |
| TAGCTTTGCC | | | 5205 |
| TACTCCAGAA | | | 5206 |
| TAGGCTCCAT | | | 5207 |
| TACCCGTACA | | | 5208 |
| TACCCAGAA | | | 5209 |
| TACCATCAA | | | 5210 |
| TACCACCAAT | | | 5211 |
| TACATATGGA | Human mRNA for KIAA0248 gene, partial cds. | D87435 | 5212 |
| TACAGCCCCC | | | 5213 |
| TACAGAGTTT | | | 5214 |
| GTGGTGCGCG | | | 5215 |
| TACTGAAACA | | | 5216 |
| TATGTAAAAT | | | 5217 |
| TCACAAAAGA | | | 5218 |
| TCAATAAAAG | | | 5219 |
| TCAAGTCCAG | | | 5220 |
| TATTTTCTGC | | | 5221 |
| TATTTATATG | Homo sapiens cig41 mRNA, partial sequence. | AF0269 | 5222 |
| TATTGTTGGT | | | 5223 |
| TATCAAAGG | | | 5224 |
| TAGCTGGGAC | | | 5225 |
| TATGTCTGCA | | | 5226 |
| TAATAAAGGC | | | 5227 |
| TATCATTATT | | | 5228 |
| TATATAAGCT | | | 5229 |
| TAGTTGAGGT | | | 5230 |
| TAGTGAAATG | Homo sapiens CASK mRNA, complete cds. | AF0355 | 5231 |
| TAGTCATCTT | | | 5232 |
| TAGTAGGGTG | | | 5233 |
| TAGGTGACTC | | | 5234 |
| TAGGGGTTTC | | | 5235 |
| TATGTGCGTG | | | 5236 |
| GTTATTTTAC | | | 5237 |
| TACAGACTCT | | | 5238 |
| GTTCCCTCCCC | | | 5239 |
| GTTCCGGAGG | Human clone X-1b mRNA from chromosome X. | U66049 | 5240 |
| GTTCCACCAG | | | 5241 |

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| GTTCCACATT | | | 5242 |
| GTTCCAAAAA | | | 5243 |
| G TTCAGTCAG | | | 5244 |
| GTTGCTAGGA | | | 5245 |
| G TTCAGAACT | H.sapiens mRNA for ORF (clone ICRFp507G2490). | Z70222 | 5246 |
| GTTGCTGAGG | | | 5247 |
| GTTATATCCA | | | 5248 |
| GTTAGAGCAG | | | 5249 |
| GTGTTCTTTG | | | 5250 |
| GTGTGAAAAA | | | 5251 |
| GTGTCCTTGT | | | 5252 |
| GTGTAGAAAT | | | 5253 |
| GTGGTTTGGC | | | 5254 |
| GGCGACCGTT | | | 5255 |
| G TTCAGCTCT | | | 5256 |
| TAAATGTTGA | Human clone 23721 mRNA sequence. | U79291 | 5257 |
| TAAGTTTAAT | Human sterol carrier protein X/sterol carrier prot | M75883 | 5258 |
| TAAGGGAGCT | | | 5259 |
| TAAGGATTTT | | | 5260 |
| TAAGCCCAAG | | | 5261 |
| TAAGCATTAA | Human scaffold protein Pbp1 mRNA, complete cds. | U83463 | 5262 |
| TAAC TTACAT | Human mRNA for KIAA0269 gene, complete cds. | D87459 | 5263 |
| TAACCATCAA | | | 5264 |
| G TTCCTTGGC | | | 5265 |
| TAAATTACCA | H.sapiens SPR-2 mRNA for GT box binding protein. | X68560 | 5266 |
| GTGGTGGATG | | | 5267 |
| TAAATAAAGG | | | 5268 |
| TAAAGCAGTA | H.sapiens mRNA for restin. | X64838 | 5269 |
| TAAAATGTTT | | | 5270 |
| TAAAAGGAGG | | | 5271 |
| GTTTGTTCAA | | | 5272 |
| GTTTGGGGGG | | | 5273 |
| GTTTCCTTTG | | | 5274 |
| GTTGTGGTAA | | | 5275 |
| TAACAAAAAT | | | 5276 |
| GCCAAGAATC | | | 5277 |
| GCCGAGGGAA | | | 5278 |
| GCCCTAGCAA | | | 5279 |
| GCCCGCAGTT | | | 5280 |
| GCCCCGGAGC | | | 5281 |
| GCCCCCTGGG | | | 5282 |

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| GCCCCCAGAT | | | 5283 |
| GCCCAGGGAC | | | 5284 |
| GCTTCCCAGC | Homo sapiens mRNA for CDEP, complete cds. | AB0084 | 5285 |
| GCCAGTCAAA | | | 5286 |
| GCCTGGCCTG | | | 5287 |
| GCCAAAGAGA | | | 5288 |
| GCATTTTGTG | | | 5289 |
| GCATCCGGAG | | | 5290 |
| GCAGCACGCT | | | 5291 |
| GCAGACATTG | | | 5292 |
| GCACCCGCCT | | | 5293 |
| GCAAGGTTGC | | | 5294 |
| GCCAGTGCCT | Human mRNA for RD protein, RNA- binding. | X16105 | 5295 |
| GCGGCGGGCGG | | | 5296 |
| CATTTTGGGG | Homo sapiens EEN-B2-L4 mRNA, complete cds. | AF0362 | 5297 |
| GCTGTAGGGG | | | 5298 |
| GCTGCCAAAA | | | 5299 |
| GCTGCAGACA | | | 5300 |
| GCTCTGGTTC | | | 5301 |
| GCTCACTGCA | Human cyclophilin-like protein CyP-60 mRNA, comple | U37219 | 5302 |
| GCTAGTGAAA | | | 5303 |
| GCCGCCTCTC | | | 5304 |
| GCGGCTGCGC | | | 5305 |
| GCCTCCAGGG | | | 5306 |
| GCGGCGCCCT | | | 5307 |
| GCGGCCAGTA | | | 5308 |
| GCGCTGCTTT | | | 5309 |
| GCGAGCTGAA | | | 5310 |
| GCCTTCTGCT | Human PL6 protein (PL6) mRNA, complete cds. | U09584 | 5311 |
| GCCTTAGGGT | | | 5312 |
| GCCTGGCTGG | Human thiazide-sensitive Na-Cl cotransporter (hTSC | U44128 | 5313 |
| GATGTGCTGG | | | 5314 |
| GCTAAACTCT | | | 5315 |
| GAATAAATTG | | | 5316 |
| GCAAATCTGA | | | 5317 |
| GACTGAGCTT | | | 5318 |
| GACTCAGCTG | | | 5319 |
| GACTATAGCG | | | 5320 |
| GACCGCCTGT | | | 5321 |
| GACCCCTAAA | | | 5322 |

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| GACCAACAGT | | | 5323 |
| GAGAACCCAG | | | 5324 |
| GAATGAAGCT | | | 5325 |
| GAGAAGCCCG | | | 5326 |
| GAATAAACAC | | | 5327 |
| GAAGGTCCTG | Human pyruvate dehydrogenase E1-beta subunit mRNA, | M34055 | 5328 |
| GAAGACGGTG | | | 5329 |
| GAACAAGCCA | | | 5330 |
| GAACAAATGG | | | 5331 |
| GAAAAATCAA | | | 5332 |
| CTTTTGTCGT | | | 5333 |
| CTTCTATGTA | Human mRNA for KIAA0177 gene, partial cds. | D79999 | 5334 |
| GACATCGAGG | | | 5335 |
| GAGCTGGTGA | | | 5336 |
| GCTTGTACCT | | | 5337 |
| GATGCATTAG | | | 5338 |
| GATCCCAAT | | | 5339 |
| GATATGAGGG | Human p21-activated protein kinase (Pak1) gene, co | U24152 | 5340 |
| GAGTTTTGTG | | | 5341 |
| GAGTCAGCAT | | | 5342 |
| GAGGGCCTTC | | | 5343 |
| GACTTGGCGG | | | 5344 |
| GAGGACCCCT | | | 5345 |
| GCAAAATAAC | Human initiation factor 4D 9eIF 4D) mRNA, complete | M23419 | 5346 |
| GAGCCTCACA | Human mRNA for KIAA0076 gene, complete cds. | D38548 | 5347 |
| GAGCACAGGT | Human protein-serine/threonine (AKT2) mRNA, comple | M95936 | 5348 |
| GAGATGGATA | | | 5349 |
| GAGAGGTCAC | Homo sapiens hyaluronidase (LUCA-3) mRNA, complete | AF0407 | 5350 |
| GAGAGGAAAC | | | 5351 |
| GAGAGCAGCC | | | 5352 |
| GAGACTTGAG | Human leukocyte adhesion protein (LFA-1/Mac-1/p150 | M15395 | 5353 |
| GAGACTGCTG | | | 5354 |
| GAGGAGCCCC | | | 5355 |
| GTGAAAGCCC | | | 5356 |
| GTGGCAGATG | | | 5357 |
| GTGGAGGTTC | Homo sapiens mRNA for putative GTP-binding protein | Y14391 | 5358 |
| GTGCTATCCT | | | 5359 |

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| GTGCCACTGC | | | 5360 |
| GTGCAGTCCT | | | 5361 |
| GTGCAGAAGC | | | 5362 |
| GTGAGTGTGT | | | 5363 |
| GCTTACAGGT | | | 5364 |
| GTGAACCCCG | | | 5365 |
| GTGGCGGGAG | H.sapiens mRNA for RAP74. | X64002 | 5366 |
| GTGAAACGCC | | | 5367 |
| GTCTGTGCAG | | | 5368 |
| GTCTAGAATC | | | 5369 |
| GTATTTAACA | | | 5370 |
| GTATGATCCT | | | 5371 |
| GTAGCAAAAA | | | 5372 |
| GGTGAGCTAC | | | 5373 |
| GTGAGACCCT | Human Myf-3 mRNA for myogenic determining factor 3 | X17650 | 5374 |
| TAAATATGCA | | | 5375 |
| TACACCAAGA | | | 5376 |
| TAATTTTTAA | H.sapiens RR2 mRNA for small subunit ribonucleotid | X59618 | 5377 |
| TAATCGAAAC | | | 5378 |
| TAATATAATT | | | 5379 |
| TAATACTCCA | | | 5380 |
| TAAGGAAGGC | Homo sapiens mRNA for KIAA0601 protein, partial cd | AB0111 | 5381 |
| TAACTCCATT | | | 5382 |
| GTGGCATCCC | | | 5383 |
| TAAATTCAAG | | | 5384 |
| GTGGCCTGTG | | | 5385 |
| TAAAGCCTTT | | | 5386 |
| GTTTGTACAA | | | 5387 |
| GTTTCTATCA | Homo sapiens clone 23797 and 23917 mRNA, partial c | AF0352 | 5388 |
| GTTTCCCCAA | | | 5389 |
| GTTAATCTGG | | | 5390 |
| GTGTTTATTA | | | 5391 |
| GTGTACTCAT | Homo sapiens serine protease (Omi) mRNA, complete | AF0207 | 5392 |
| GGTCCAAAAT | | | 5393 |
| TAACAAACCT | | | 5394 |
| GGACTTTCCT | Human mRNA for RTP, complete cds. | D87953 | 5395 |
| GGTGAAACCC | | | 5396 |
| GGCAACAGAG | Homo sapiens clone HEA6 Cri-du-chat region mRNA. | AF0092 | 5397 |
| GGCAAAACCA | | | 5398 |
| GGATGTGGAG | | | 5399 |

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| GGATGCGCAG | | | 5400 |
| GGATCCAAGT | | | 5401 |
| GGAGTCCTAG | Ig V kappa =anti-single/double-stranded DNA antibo | S59162 | 5402 |
| GGAAGTTCAA | H.sapiens unusual BuChE mRNA. | X52767 | 5409 |
| GGAAGGGTGT | | | 5410 |
| GGAAGGGGAA | | | 5411 |
| GGAAAGCCAG | | | 5412 |
| GGAAAAATGG | | | 5413 |
| GGAGGTGGAG | Human clone AZA3 Alu repeat sequence. | U02046 | 5414 |
| GGGCCCCGTAC | | | 5415 |
| CTTAATAAAA | | | 5416 |
| GGGTTTTATA | | | 5417 |
| GGGTTCCCCG | | | 5418 |
| GGGGGCGCCT | | | 5419 |
| GGGGGCAGGG | | | 5420 |
| GGGCTCCAGG | | | 5421 |
| GGGCGCCTCC | | | 5422 |
| GGCACCGTGG | | | 5423 |
| GGGCCGTGGG | | | 5424 |
| GGTCCCGTTC | | | 5425 |
| GGGCAACGTG | | | 5426 |
| GGGAGGAACA | | | 5427 |
| GGCTCTCCCT | | | 5428 |
| GGCGAAACCC | | | 5429 |
| GGCCCAGCTG | | | 5430 |
| GGCCAGTGTT | | | 5431 |
| GGCATCAAGT | | | 5432 |
| GGCAGGGCTG | | | 5433 |
| GGGCCTAAAC | | | 5434 |
| AGGCCAGGAG | | | 5435 |
| ATCACTTGGG | | | 5436 |
| ATATGAAGCA | | | 5437 |
| ATATACTGTA | | | 5438 |
| ATACTTACAT | | | 5439 |
| ATACATAATA | | | 5440 |
| AGTTTATGCC | | | 5441 |
| AGTTGTATAT | | | 5442 |
| CTTCCTGTAT | | | 5443 |

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| AGGGAAGCTG | | | 5444 |
| ATCATTTGTT | | | 5445 |
| AGGCAGGGAC | | | 5446 |
| AGGCAGGCTC | | | 5447 |
| AGGCAGACGG | | | 5448 |
| AGGAGATGGA | Homo sapiens clk3 mRNA, complete cds. | L29217 | 5449 |
| AGGACAGAAG | | | 5450 |
| AGCTGACCCG | | | 5451 |
| AGCTCTATGA | | | 5452 |
| AGGTGGCAAC | | | 5453 |
| ATGGCAGGCG | | | 5454 |
| ATGTTTCAGGC | | | 5455 |
| ATGTGATTGT | Human mRNA for PIG-F (phosphatidyl-inositol-glycan | D13435 | 5456 |
| ATGTAAAGTG | | | 5457 |
| ATGGTGACTC | | | 5458 |
| ATGGCTGGGT | | | 5459 |
| ATGGCGTTTC | | | 5460 |
| TTTTTTTTTT | Human p55CDC mRNA, complete cds. | U05340 | 5461 |
| ATCAGTATGT | | | 5462 |
| TTGGGGTTTC | Human mRNA for apoferritin H chain type. | X00318 | 5463 |
| ATCATACCAC | | | 5464 |
| ATGCCTTTGA | Human mRNA for cGMP-dependent protein kinase type | D45864 | 5465 |
| ATGCCCCGAGG | | | 5466 |
| ATGCAGCCGT | | | 5467 |
| ATGAGGGTCC | | | 5468 |
| ATGAGCGTCT | | | 5469 |
| ATGACCTGAA | | | 5470 |
| ATCTGAGGTT | | | 5471 |
| AGCCACGTTG | Human adipocyte acid phosphatase mRNA. | M87545 | 5472 |
| ATGGCCGGTA | | | 5473 |
| ACAGCCCATT | | | 5474 |
| AGCGCCGATG | | | 5475 |
| ACGTGGAGCT | | | 5476 |
| ACGTGCCTCA | | | 5477 |
| ACGCAACAGG | | | 5478 |
| ACCTTATCAA | H.sapiens Mpv17 mRNA. | X76538 | 5479 |
| ACCCGCGGTA | | | 5480 |
| ACCACAGCAA | | | 5481 |
| ACTCCAAGGA | | | 5482 |
| ACATAGAGTG | | | 5483 |
| ACTCCTTCCT | | | 5484 |

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| ACAGACACAA | | | 5485 |
| ACACAGATTT | | | 5486 |
| ACAACACCCC | Homo sapiens mRNA for inositol 1,4,5-trisphosphate | D38169 | 5487 |
| ACAAACAAAA | | | 5488 |
| AATTTTCAGT | | | 5489 |
| AATTGTGCAT | | | 5490 |
| AATTCAGTGA | Human CW-1 mRNA, complete cds. | U56255 | 5491 |
| AATGTCATTG | | | 5492 |
| ACATTGGTAA | | | 5493 |
| AGAATTTGCA | | | 5494 |
| ATTTAAAAAA | | | 5495 |
| AGCATCTAAC | | | 5496 |
| AGCAGGCTCA | | | 5497 |
| AGCAGGAGCC | | | 5498 |
| AGCACCTCCC | | | 5499 |
| AGAGAGAGTC | | | 5500 |
| AGAGACTCTT | | | 5501 |
| ACTACTAAAT | | | 5502 |
| AGACAGTAAT | | | 5503 |
| AGCCAGCCAC | | | 5504 |
| AGAAATGTGA | | | 5505 |
| ACTTTTGCCC | | | 5506 |
| ACTTTGTGGG | | | 5507 |
| ACTTGAAAGG | | | 5508 |
| ACTTATGTTT | | | 5509 |
| ACTGCAGAGC | | | 5510 |
| ACTGAAAGGC | | | 5511 |
| ACTCTAAGTG | | | 5512 |
| AGACCCTGTC | | | 5513 |
| CGCAGGCACC | | | 5514 |
| CCGGAAACAC | | | 5515 |
| CTAGAAAGGT | | | 5516 |
| CTAAGATTCA | | | 5517 |
| CGTTTAATCA | | | 5518 |
| CGTGTGTGCC | | | 5519 |
| CGGTCCCGTT | | | 5520 |
| CGGCAAAAAA | | | 5521 |
| CTAGCGCGTG | | | 5522 |
| CGCGCACCCG | | | 5523 |
| CTATCAGTTT | Homo sapiens dynein light intermediate chain 2 (LI) | AF0358 | 5524 |
| CGCAACTGCG | | | 5525 |
| CCTGTTATCC | | | 5526 |
| CCTGTAGATG | | | 5527 |
| CCTGGCCATC | | | 5528 |

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| CCTGCACACT | | | 5529 |
| CCTCTGTCCC | | | 5530 |
| CCTCCTGGGG | | | 5531 |
| ATTCCTGACC | Homo sapiens PHD Finger 1 (PHF1) mRNA, complete cd | AF0296 | 5532 |
| CGGACAATCA | | | 5533 |
| CTGCTGTAAT | | | 5534 |
| TACAGAGCTC | | | 5535 |
| CTGTGCCCCA | | | 5536 |
| CTGTATTTGA | Human transformer-2 alpha (htra-2 alpha) mRNA, com | U53209 | 5537 |
| CTGGGGCCTG | | | 5538 |
| CTGGGGAGGG | | | 5539 |
| CTGGCCGACT | Human proline and glutamic acid rich nuclear prote | U88154 | 5540 |
| CTGGAGACTC | | | 5541 |
| CTAGAGAACT | | | 5542 |
| CTGGACCACT | | | 5543 |
| CCGCCTTCGG | | | 5544 |
| CTGCCCTGGA | Homo sapiens clone NBB9 Cri-du-chat region mRNA. | AF0092 | 5545 |
| CTGCAAGTTC | | | 5546 |
| CTGACCCCCT | | | 5547 |
| CTGAATTCCC | | | 5548 |
| CTCATATGTT | | | 5549 |
| CTCATAAGGG | | | 5550 |
| CTCACCGCCC | Human cellular retinoic acid-binding protein II (C | M68867 | 5551 |
| CTATTTAGTT | Human alpha-L-fucosidase, complete cds. | M29877 | 5552 |
| CTGGACTGGG | | | 5553 |
| CACCAAACCT | | | 5554 |
| CCGGCCGCCT | | | 5555 |
| CATACTTCAA | | | 5556 |
| CAGGGCGGGT | Human Hsp27 ERE-TATA-binding protein (HET) mRNA, c | U72355 | 5557 |
| CAGGCATCCC | | | 5558 |
| CAGGATGACG | | | 5559 |
| CAGATAACAT | Human mRNA for KIAA0016 gene, complete cds. | D13641 | 5560 |
| CACTTTCAAG | | | 5561 |
| CCACGGCACT | | | 5562 |
| CACCTAACTG | | | 5563 |
| CCACTCTTGA | | | 5564 |
| CACACCCCTG | H.sapiens mRNA for putative progesterone binding p | Y12711 | 5565 |

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| CACACAGCAC | | | 5566 |
| CACAAACTGA | | | 5567 |
| CAAGGTGAAA | | | 5568 |
| CAACTGGAGT | Human mRNA for KIAA0384 gene, complete cds. | AB0023 | 5569 |
| CAAAGGCAGC | | | 5570 |
| ATTTTTTCAA | H.sapiens mRNA for PAPS synthetase. | Y10387 | 5571 |
| CTTCAACATC | | | 5572 |
| CACCTAATGG | | | 5573 |
| CCCACAATCC | | | 5574 |
| CCCTTCGAGA | | | 5575 |
| CCCTAATTGC | | | 5576 |
| CCCCTGGGAC | | | 5577 |
| CCCCCAATTC | | | 5578 |
| CCCCATCGGT | | | 5579 |
| CCCCAAGGTG | | | 5580 |
| CCCAGCCACA | | | 5581 |
| CATTTAAGTT | H.sapiens mRNA for protein induced by vitamin D. | X98091 | 5582 |
| CCCACCGTCC | | | 5583 |
| ATTCTTACAG | | | 5584 |
| CCATTCTCCT | | | 5585 |
| CCATACAGAA | | | 5586 |
| CCAGTTTTGC | | | 5587 |
| CCAGCAAGAG | | | 5588 |
| CCAGAATCTT | | | 5589 |
| CCACTTCCAA | | | 5590 |
| CCACTTCACT | | | 5591 |
| CCACTGTGCT | | | 5592 |
| CCCACTGCCC | | | 5593 |
| AGCCACCTCC | | | 5594 |
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| AGCTGCTTCA | | | 5596 |
| AGCGTGGAGG | | | 5597 |
| AGCGGAAGAG | | | 5598 |
| AGCCTGGGAG | | | 5599 |
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| AGCCCTACGA | | | 5601 |
| ACACATATTA | | | 5602 |
| AGCCAGATCC | | | 5603 |
| AGGATGAGGG | | | 5604 |
| AGCAGCTTCT | | | 5605 |
| AGCAGCGGGG | | | 5606 |
| AGCAGATTCA | | | 5607 |
| AGCAGATCCA | | | 5608 |

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|------------|---|--------|------|
| AGATTGGTGA | | | 5609 |
| AGATTCAGAG | | | 5610 |
| AGATGGGCGA | | | 5611 |
| AGCCCACCGC | | | 5612 |
| AGTCAGCTGG | Human epidermal growth factor receptor kinase subs | U12535 | 5613 |
| ATAATACCAG | | | 5614 |
| ATAAAGCCGA | | | 5615 |
| AGTTCCTGGT | | | 5616 |
| AGTTCCAGGA | | | 5617 |
| AGTGTATTTT | Human cation-independent mannose 6-phosphate recep | J03528 | 5618 |
| AGTGCACGTG | | | 5619 |
| AGTCTCCCCT | Human putative chromatin structure regulator (SUPT | U46691 | 5620 |
| AGGAAACGAG | | | 5621 |
| AGTCCAATGG | | | 5622 |
| AGGAATGTTA | | | 5623 |
| AGGTCCCCTG | | | 5624 |
| AGGTCAGAGG | | | 5625 |
| AGGGGAAGGT | | | 5626 |
| AGGGCAGTAC | | | 5627 |
| AGGCGGCAAG | | | 5628 |
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| AGGATGGCGG | | | 5630 |
| AGAGGTTGAT | | | 5631 |
| AGTCCTAATG | | | 5632 |
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| AGATGGCAAG | | | 5634 |
| ACGGCCTGGT | | | 5635 |
| ACGCCCCAAC | | | 5636 |
| ACGACGACCG | | | 5637 |
| ACCTGTTCCC | | | 5638 |
| ACCTCCACCA | Human RNA polymerase II subunit hsRPB4 mRNA, compl | U85510 | 5639 |
| ACCGTAAGTA | | | 5640 |
| ACGTCATCGA | | | 5641 |
| ACCCCTACAA | | | 5642 |
| ACTATAATCC | | | 5643 |
| ACCCCAAAAA | | | 5644 |
| ACCAGCCTGG | | | 5645 |
| ACCACTGGAA | | | 5646 |
| ACATCTTGCT | Human NIMA-like protein kinase 1 (NLK1) mRNA, comp | U11050 | 5647 |
| ACATCACTAA | | | 5648 |
| ACAGCTCCCC | | | 5649 |

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|------------|--|--------|------|
| ACAGCAAGTT | | | 5650 |
| TACACTTGCC | | | 5651 |
| ACCCTTACAA | | | 5652 |
| AGAAATAAAT | | | 5653 |
| ATATCAATAA | | | 5654 |
| AGAGAGAGAG | | | 5655 |
| AGACGCTTCT | Homo sapiens FRG1 mRNA, complete cds. | L76159 | 5656 |
| AGACGCGGCT | | | 5657 |
| AGAATAACTG | | | 5658 |
| AGAAGTATGA | | | 5659 |
| AGAAGTAGTG | | | 5660 |
| ACGTCAGATC | | | 5661 |
| AGAAGGAAGG | | | 5662 |
| AGATAAAGAC | | | 5663 |
| ACTTTTTTAT | | | 5664 |
| ACTTTGGTTT | Homo sapiens mRNA for colon cancer clone PM208. | Y13810 | 5665 |
| ACTGGGTAAA | | | 5666 |
| ACTGATGCAA | | | 5667 |
| ACTGATAACA | | | 5668 |
| ACTCTTGACA | | | 5669 |
| ACTCAGATGC | | | 5670 |
| ACTATTTTAC | | | 5671 |
| AGAAGGAGAG | | | 5672 |
| CAATAAAATG | | | 5673 |
| ATTTTGTCCC | H.sapiens mRNA for MHC class I promoter binding pr | X65463 | 5674 |
| CACGCGGGGG | | | 5675 |
| CACGAAGATG | Human (memc) mRNA, 3'UTR. | U30999 | 5676 |
| CACCCCTCAG | | | 5677 |
| CACACCTCCC | H.sapiens mRNA for B cell membrane protein CD22. | X59350 | 5678 |
| CACACAGATC | | | 5679 |
| CACACACAAA | | | 5680 |
| CACTACTCTG | | | 5681 |
| CACAAAACGG | | | 5682 |
| CACTCATTA | | | 5683 |
| CAATAAAACT | | | 5684 |
| CAAGGAACAG | | | 5685 |
| CAACCATCCA | | | 5686 |
| CAACACTGTG | | | 5687 |
| CAACAATGTC | | | 5688 |
| CAAATAAACC | H.sapiens mRNA for Pirin, isolate 1. | Y07867 | 5689 |
| CAAACATTTG | | | 5690 |
| ATAATTCTTG | | | 5691 |

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|------------|---|--------|------|
| CACAACGGTA | | | 5692 |
| CAGGGCGAGA | | | 5693 |
| CATTGTGGAG | | | 5694 |
| CATTGCCTTC | | | 5695 |
| CATTCATAAC | | | 5696 |
| CATTCAACAT | | | 5697 |
| CATCTGTACT | Human MHC HLA-Dw12 mRNA, complete cds. | M57648 | 5698 |
| CATCTGAGAT | | | 5699 |
| CATCCTTGGG | | | 5700 |
| CACTACCCAC | | | 5701 |
| CAGTAAATGA | | | 5702 |
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| CAGAAGCACA | | | 5708 |
| CAGAAGAAAA | | | 5709 |
| CAGAAAAGCA | | | 5710 |
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| CATATTCAGT | | | 5712 |
| ATCCTGTCAC | | | 5713 |
| CAAAAGATTA | | | 5714 |
| ATGCGGCCAC | | | 5715 |
| ATGCCTTTTT | H.sapiens mRNA for NBK apoptotic inducer protein. | X89986 | 5716 |
| ATGCCAGCTG | | | 5717 |
| ATGACTGTAC | H.sapiens mRNA for C1D protein. | X95592 | 5718 |
| ATCTTGCCCT | | | 5719 |
| ATCTTCTAAA | | | 5720 |
| ATGGCAGGGC | Homo sapiens mRNA for homeodomain protein Prep-1. | Y13613 | 5721 |
| ATCGGCTCCC | | | 5722 |
| ATGGCGCCTC | | | 5723 |
| ATCCTCCAGT | | | 5724 |
| ATCCGCGGGG | | | 5725 |
| ATCAAGGTGT | | | 5726 |
| ATCAACTGGA | H.sapiens mRNA for NEFA protein. | X76732 | 5727 |
| ATCAAAGAGT | | | 5728 |
| ATATGTGGTC | | | 5729 |
| ATATGGAATA | | | 5730 |
| ACACAGCAGG | | | 5731 |
| ATCTCAGCTC | Homo sapiens TNF receptor associated factor 5 mRNA | U69108 | 5732 |
| ATTCCATCTG | | | 5733 |

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|------------|--|--------|------|
| ATTTTCCTTA | | | 5734 |
| ATTTTCAAGA | | | 5735 |
| ATTTGTCCCC | | | 5736 |
| ATTGCACCAG | | | 5737 |
| ATTCTTTTTA | | | 5738 |
| ATTCTTCTGA | Human dystrophin-related protein 2 (DRP2) mRNA, co | U43519 | 5739 |
| ATTCTCCAGG | | | 5740 |
| ATGGCAACAG | Human channel-like integral membrane protein (AQP- | U41518 | 5741 |
| ATTCCCCAGT | | | 5742 |
| ATACAGTAGT | | | 5743 |
| ATTAAAGTCA | Human mRNA for KIAA0237 gene, complete cds. | D87074 | 5744 |
| ATGTTTACAC | Human pre-T/NK cell associated protein (5A3) mRNA. | L17329 | 5745 |
| ATGTTAGATA | | | 5746 |
| ATGTGTTCTA | | | 5747 |
| ATGTGAGGGA | | | 5748 |
| ATGGTGAGTG | | | 5749 |
| ATGGCTTTGT | | | 5750 |
| ATGGCGGCGA | | | 5751 |
| ATTCGGTTAG | | | 5752 |
| TGCAGAAACA | | | 5753 |
| TGGAAGCTAG | | | 5754 |
| TGGAATAAAA | upstream stimulatory factor=transcription factor [| S50537 | 5755 |
| TGCTGTTGCT | | | 5756 |
| TGCTACGAAA | | | 5757 |
| TGCCTGCTTG | | | 5758 |
| TGCCTATAGC | | | 5759 |
| TGCCCAGCAA | Homo sapiens G protein-coupled receptor kinase 6, | AF0407 | 5760 |
| ACACGTACTA | | | 5761 |
| TGCAGACCCA | Human tax1-binding protein TXBP151 mRNA, complete | U33821 | 5762 |
| TGGCTAGATT | | | 5763 |
| TGCACTTGAC | | | 5764 |
| TGATTTCCAC | | | 5765 |
| TGATTGGTGG | Human platelet-derived growth factor alpha-recepto | L25829 | 5766 |
| TGATCTGGGA | | | 5767 |
| TGAGTTTTAC | | | 5768 |
| TGAAGGTGGT | | | 5769 |
| TGAAATCTGA | | | 5770 |
| TGCAGTGTGC | | | 5771 |

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|------------|--|--------|------|
| TGCTTTTATA | | | 5772 |
| TTAGGTGATG | | | 5773 |
| TTACCGTCCC | | | 5774 |
| TTACAGTGTT | Homo sapiens protein phosphatase 2A B56-epsilon (P | L76703 | 5775 |
| TTAAGACCCT | | | 5776 |
| TTAAACTCCA | | | 5777 |
| TGTGTGAGCT | | | 5778 |
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| TGTGCGCGTG | | | 5781 |
| TGGCCACGGC | | | 5782 |
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| TGTATTCAGC | | | 5784 |
| TGTATGTAAA | | | 5785 |
| TGTAAGAACA | | | 5786 |
| TGGGTAGGAG | | | 5787 |
| TGGGGTGGAG | Human glutathione transferase Zeta 1 (GSTZ1) mRNA, | U86529 | 5788 |
| TGGGGCGTGC | | | 5789 |
| TCTGCCTCGT | | | 5790 |
| TGTGCTGTTT | Human PML-1 mRNA, complete CDS. | M79462 | 5791 |
| TCAAAGTATA | | | 5792 |
| TCTTTGGCCT | | | 5793 |
| TCACTGCATT | | | 5794 |
| TCACTGAGTT | | | 5795 |
| TCACGGCAAG | | | 5796 |
| TCACCGTACA | | | 5797 |
| TCAATAAATG | | | 5798 |
| TCAAGCATCC | | | 5799 |
| TCAGACTTTT | | | 5800 |
| TCAAATCACA | | | 5801 |
| TCAGATGAAA | | | 5802 |
| TATGAAGCCG | | | 5803 |
| TATATTGATT | Human BTG1 mRNA. | X61123 | 5804 |
| TAGTTTCAAC | Human mRNA for cyclin I, complete cds. | D50310 | 5805 |
| TAGTCAGGTA | Human mRNA for acetyl-coenzyme A transporter, comp | D88152 | 5806 |
| TAGTAAGTCA | | | 5807 |
| TAGGTCTCTT | | | 5808 |
| TACTGTAGTC | | | 5809 |
| AATGATGTTC | | | 5810 |
| TCAAATTAAA | | | 5811 |
| TCCTGAAAAA | | | 5812 |
| TTATGCCTCC | | | 5813 |

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|-------------|--|--------|------|
| TCTGACAAAC | | | 5814 |
| TCTCTGCTGC | | | 5815 |
| TCTCAAGTAA | | | 5816 |
| TCTAGTCACT | | | 5817 |
| TCTAGAATTT | | | 5818 |
| TCCTTTTTC | Human tyrosyl-tRNA synthetase mRNA, complete cds. | U40714 | 5819 |
| TCACTGTGGG | Human nonerythroid alpha-spectrin (SPTAN1) mRNA, c | J05243 | 5820 |
| TCCTGAAATA | | | 5821 |
| TCTTTAGTTG | | | 5822 |
| TCCTCATCCT | Human p18 protein mRNA, complete cds. | J04991 | 5823 |
| TCCGGCTCTC | | | 5824 |
| TCCCTTATTA | | | 5825 |
| TCCCCGTTAC | | | 5826 |
| TCCAGCAGCT | | | 5827 |
| TCAGTGC GCA | | | 5828 |
| TCAGGTGTTA | | | 5829 |
| TCAGCTGGGG | | | 5830 |
| TCCTGGCTGC | | | 5831 |
| AACGGGGCCC | Human macrophage-derived chemokine precursor (MDC) | U83171 | 5832 |
| AAATCTGGCA | Human I-plastin mRNA, complete cds. | L20826 | 5833 |
| AAGCAGATCA | | | 5834 |
| AAGACAGTAG | | | 5835 |
| AAGAACAGTG | | | 5836 |
| AACTGTATAC | Human MHC class II gene. | M84748 | 5837 |
| AACTGAGGTG | | | 5838 |
| AACTCTGGGT | | | 5839 |
| AAGCCTGTAG | | | 5840 |
| AACTCTAAGG | | | 5841 |
| AAGCTTCTCA | | | 5842 |
| AACGCTGGCC | | | 5843 |
| AACCTTCCTC | | | 5844 |
| AACATCAAAC | Homo sapiens Arp2/3 protein complex subunit p16-Ar | AF0060 | 5845 |
| AACATACACA | | | 5846 |
| AACAGAATAT | | | 5847 |
| AACACTCGTA | | | 5848 |
| AACAAATTCT | | | 5849 |
| TTAGTCTTCA | | | 5850 |
| AACTCTGGAC | | | 5851 |
| AATCTTGAGT | | | 5852 |
| AATTTAGGCA | Human mRNA for coproporphyrinogen oxidase, complet | D16611 | 5853 |

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|-------------|---|--------|------|
| AATTGTGCAG | | | 5854 |
| AATTGCAAGC | Human cofilin mRNA. | D00682 | 5855 |
| AATTCTCCAT | | | 5856 |
| AATTGCGATTG | | | 5857 |
| AATTCATAGG | | | 5858 |
| AATTATCAAC | | | 5859 |
| AAGCCTAAAA | Human breast cancer, estrogen regulated LIV-1 prot | U41060 | 5860 |
| AATGAAATAA | | | 5861 |
| AAAGGAAAAT | | | 5862 |
| AATCTCAGAC | | | 5863 |
| AATCCTTTGG | | | 5864 |
| AAGGGCCACT | | | 5865 |
| AAGGCTAACG | | | 5866 |
| AAGGCGGAGG | | | 5867 |
| AAGGCCCGAG | | | 5868 |
| AAGGCAGAGA | | | 5869 |
| AAGGAATGGG | | | 5870 |
| AATGGGTGAA | | | 5871 |
| TTCTGTGCTG | Human mRNA for complement component C1r. | X04701 | 5872 |
| AAATTTTAAT | | | 5873 |
| TTGCCGGTTT | | | 5874 |
| TTGCAACCAA | | | 5875 |
| TTGAGAACTG | | | 5876 |
| TTGACCCAGC | | | 5877 |
| TTGAGAGAGG | | | 5878 |
| TTGAATTGGG | | | 5879 |
| TTGGCCAGAC | Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complet | U09215 | 5880 |
| TTCTTGTTGGG | | | 5881 |
| TTGGCCCTCT | | | 5882 |
| TTCTGTAGCC | H.sapiens mRNA for adenosine triphosphatase, calci | Z69881 | 5883 |
| TTCTCATAGG | | | 5884 |
| TTCTCATAAT | | | 5885 |
| TTCTTGCTAC | | | 5886 |
| TTCCCGAGGG | | | 5887 |
| TTCCCAAGGG | | | 5888 |
| TTCATATTAA | | | 5889 |
| TACAGAACAC | | | 5890 |
| TTGAATTCCC | Human mRNA for semaphorin E, complete cds. | AB0002 | 5891 |
| TTTCAATGCC | | | 5892 |
| AAAGAAGCCA | | | 5893 |
| AAACCCAAGC | | | 5894 |

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|------------|--|--------|------|
| AAAATTGGCT | | | 5895 |
| AAAATATTAC | Human G protein gamma-10 subunit mRNA, complete cd | U31383 | 5896 |
| AAAATACTGA | | | 5897 |
| AAAACCTGTA | | | 5898 |
| AAAAACTTTT | | | 5899 |
| TTGGCATTGT | | | 5900 |
| TTTGGTCCTC | | | 5901 |
| TTATACAGCC | | | 5902 |
| TTTATTGAAA | | | 5903 |
| TTTAGGGGGA | | | 5904 |
| TTTAAAAGAG | Human mRNA for KIAA0105 gene, complete cds. | D14661 | 5905 |
| TTGTGATTAA | | | 5906 |
| TTGGTCCCCT | | | 5907 |
| TTGGGTTGTT | | | 5908 |
| TTGGGGTTGG | | | 5909 |
| TTGGCCTGGC | | | 5910 |
| TTTTCTGTGG | | | 5911 |

CLAIMS

1. An isolated population of polynucleotides comprising or
5 corresponding to at least one polynucleotide selected from the group consisting
of SEQ ID NOS. 1 through 5911 and their respective complements.

2. A population of polynucleotides comprising or corresponding to a
population of tags selected from the group 1-5, 1-17, 18-24, 1-24, 25-36, 1-36,
18-36, 37-53, 54-74, 37-74, 1-53, 1-74, 75-116, 1-116, 117-279, 1-279, 280-
10 549, 1-549, 550-1160, 1-1160, 1161-3175, 1-3175, 3176-3183, 3184-3197,
3176-3197, 3198-3204, 3176-3204, 3205-3213, 3176-3213, 3214-3226, 3176-
3226, 3227-3242, 3176-3242, 3243-3294-3176-3294, 3295-3381, 3176-3381,
3382-3554, 3176-3354, 3555-4012, 3176-4012, 4013-5911-3176-5911, 1-
5911, or any combination thereof.

15 3. The population of claim 1, wherein the one polynucleotide
comprises or corresponds to a novel tag or its complement.

4. The population of claim 1, wherein the one polynucleotide
comprises or corresponds to a tag or its complement that is overexpressed in
cells derived from a primary breast tumor.

20 5. The complement of the polynucleotide of claims 1 or 2.

6. An isolated novel polypeptide expressed by a polynucleotide of
claim 5.

7. A solid phase support comprising a polynucleotide of claims 1
or 2,

25 8. An array of probes comprising a polynucleotide of claims 1 or
2 bound to a chip.

9. A method of aiding in the diagnoses of the metastatic condition
of a metastatic breast cell comprising determining differential expression of a
polynucleotide of claims 1 or 2, or the encoded polypeptide.

30 10. A method of modulating the genotype of a breast cell,
comprising introducing into the breast cell a polynucleotide of claim 1.

11. A method of screening for a candidate therapeutic agent that modulates the expression of a polynucleotide associated the metastatic condition of a breast cell, comprising contacting a cell with an effective amount of a potential agent, and assaying for a change in expression level of a polynucleotide of claims 1 or 2, wherein a change in the expression level is indicative of a candidate therapeutic agent.

12. A polynucleotide comprising a promoter sequence derived from a polynucleotide of claim 1.

13. A host cell comprising the polynucleotide of claim 1 or 12.

10 14. A gene delivery vehicle comprising a polynucleotide of claim 1 or 12.

15. A polynucleotide of claim 12 and a second polynucleotide operatively linked thereto.

16. A polynucleotide of claim 15, wherein the second polynucleotide encodes an antigenic peptide.

17. A method for inducing an immune response in a subject comprising administering an effective amount of the polynucleotide of claim 1, 12 or 16, to the subject.

**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**

International application No.
PCT/US99/13647

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(5): C07H 21/00; C12Q 1/68; A61K 48/00
US Cl.: 536/23.1, 24.3; 435/6, 320.1, 325; 530/350

4. Further Comments (Continued):

Claims 1-17 are directed to polynucleotides "comprising or corresponding to" specific decanucleotides set forth by SEQ ID NO, and the application does not comply with the requirements regarding nucleotide sequence disclosures. Claim 6 is directed to polypeptides encoded by the polynucleotides and the description does not disclose such polypeptides. Claims 12-17 are directed to promoters derived from the polynucleotides and the description does not disclose such polypeptides. The polynucleotides disclosed are only decanucleotides, which are incapable of encoding a polypeptide or serving as a promoter.

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| (51) International Patent Classification ⁵ : C07H 21/00, C12Q 1/68, A61K 48/00 | A2 | (11) International Publication Number: WO 99/65928 (43) International Publication Date: 23 December 1999 (23.12.99) | | | | | | | | | | | | | | | | | | |
| (21) International Application Number: PCT/US99/13647 (22) International Filing Date: 18 June 1999 (18.06.99) (30) Priority Data: <table border="0"><tr><td>60/090,039</td><td>19 June 1998 (19.06.98)</td><td>US</td></tr><tr><td>60/090,040</td><td>19 June 1998 (19.06.98)</td><td>US</td></tr><tr><td>60/090,041</td><td>19 June 1998 (19.06.98)</td><td>US</td></tr><tr><td>60/089,853</td><td>19 June 1998 (19.06.98)</td><td>US</td></tr><tr><td>60/089,997</td><td>19 June 1998 (19.06.98)</td><td>US</td></tr></table> (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application <table border="0"><tr><td>US</td><td>Not furnished (CIP)</td></tr><tr><td>Filed on</td><td>Not furnished</td></tr></table> (71) Applicant (for all designated States except US): GENZYME CORPORATION [US/US]; Metrowest Place, 15 Pleasant Street Connector, Framingham, MA 01701-9322 (US). (71)(72) Applicants and Inventors: ROBERTS, Bruce, L. [US/US]; 26 Windsor Road, Milford, MA 01757 (US). SHANKARA, Srinivas [US/US]; 24 Stoney Hill Road, Shrewsbury, MA 01545 (US). | 60/090,039 | 19 June 1998 (19.06.98) | US | 60/090,040 | 19 June 1998 (19.06.98) | US | 60/090,041 | 19 June 1998 (19.06.98) | US | 60/089,853 | 19 June 1998 (19.06.98) | US | 60/089,997 | 19 June 1998 (19.06.98) | US | US | Not furnished (CIP) | Filed on | Not furnished | (74) Agents: KONSKI, Antoinette, F. et al.; Baker & McKenzie, 660 Hansen Way, Palo Alto, CA 94304 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority.</i> |
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| 60/090,040 | 19 June 1998 (19.06.98) | US | | | | | | | | | | | | | | | | | | |
| 60/090,041 | 19 June 1998 (19.06.98) | US | | | | | | | | | | | | | | | | | | |
| 60/089,853 | 19 June 1998 (19.06.98) | US | | | | | | | | | | | | | | | | | | |
| 60/089,997 | 19 June 1998 (19.06.98) | US | | | | | | | | | | | | | | | | | | |
| US | Not furnished (CIP) | | | | | | | | | | | | | | | | | | | |
| Filed on | Not furnished | | | | | | | | | | | | | | | | | | | |
| (54) Title: POLYNUCLEOTIDE POPULATION ISOLATED FROM NON-METASTATIC AND METASTATIC BREAST TUMOR TISSUES | | | | | | | | | | | | | | | | | | | | |

*(Referred to in PCT Gazette No. 25/2000, Section II)

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| | | | |
| (57) Abstract | | | |
| <p>An expression vector containing a gene which codes for a transcription or translation product which is therapeutically active, wherein this gene is under the control of an expression control region having the sequence SEQ ID NO:1 or a fragment thereof which comprises at least the bases bp -224 to -214 and/or -197 to -207 from SEQ ID NO:1 is tumour-cell-specific and suitable for in vivo and in vitro ablation or regression of tumour cells.</p> | | | |

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Tumour-specific expression control region and the use thereof

The invention concerns a tumour-specific expression control region, vectors containing this region and its use especially for in vivo expression.

The specific expression of tumoricidal foreign genes in tumours is a promising approach for the therapeutic treatment of tumour diseases.

5 The structure and the promoter analysis of the gene which codes for the human melanoma-inhibiting protein MIA (also referred to as CD-RAP) is known from Bosserhoff, A.K., et al., J. Biol. Chem. 271 (1996) 490-495. MIA is expressed in melanoma cell lines and has growth-inhibiting effects on melanoma cells in vitro (Bogdahn et al., Cancer Res. 49 (1989) 5358-5363; International Application No. 10 WO 95/03328). Furthermore it is known from Bosserhoff and WO 95/03328 that a region of about 500 base pairs of the 5' untranslated region of the MIA gene causes the expression of MIA in malignant melanoma cells.

From Kondo, S., et al., 44th Annual Meeting, Orthopaedic Research Society, March 16-19, 1998, New Orleans, Louisiana, p. 178-30 it is known that IGF-I regulates 15 CD-RAP gene expression via an AP-2 binding site (bp -475 to -458).

From Xie, W.F., 44th Annual Meeting, Orthopaedic Research Society, March 16-19, 1998, New Orleans, Louisiana, p. 207-35 it is known that a 2.2 kb CD-RAP promoter fragment causes expression of lacZ in transgenic mice. A blue 20 colouration shows that all regulatory elements of CD-RAP are present in order to determine the natural CD-RAP expression.

Bosserhoff et al., Proc. Am. Association for Cancer Research Annual Meeting 39 (1980) p. 250, XP002087909, Abstract 1711, and Lederer et al., J. Dermatol. Sci. 16 (1998) Suppl. 1 S48, describe that a region of about 30 bp lying within the region -210 to -1 for the expression control region of the MIA gene is responsible for the 25 tumor-specific expression pattern. However, the authors do not describe the region itself.

Bosserhoff et al., Proc. Am. Association for Cancer Research Annual Meeting 37 (1996) p. 512, Abstract 3565, describe that a 300 bp partial region of the MIA expression control region is melanoma-specifically active. However, the authors do not mention that the MIA promoter has a tumor specificity.

- 5 The object of the invention is to improve the MIA promoter so that it is able in vivo to express genes specifically in tumour cells.

The object is achieved by a tumour-cell-specific expression vector containing a gene which codes for a transcription or translation product that is therapeutically active in tumour cells wherein this gene is under the control of an expression control region of the SEQ ID NO:1 or a fragment thereof which comprises at least
10 bp -224 to -214 and/or -197 to -207 from SEQ ID NO:1. Preferably, the segment is bp -224 to -197 of said sequence.

Details of the numbering of the bases (e.g. bp -224) correspond to the numbering system for expression control sequences (upstream numbering) familiar to a
15 person skilled in the art. The following classification applies:

| SEQ ID NO:1 | upstream numbering system |
|-------------|---------------------------|
| 1 | -380 |
| 157 | -224 |
| 184 | -197 |
| 380 | -1 |

Hence according to the invention "bp -224 from SEQ ID NO:1" means the base or the base pair (bp) 157 from SEQ ID NO:1 in the single or double strand.

20 Surprisingly, it has turned out that such a vector enables a tumour-specific expression of therapeutically active genes in tumour cells, which enable exclusive expression of therapeutically effective translation- or transcription products in tumour cells.

An expression control region is understood as a nucleic acid region which causes the expression of DNA and hence transcription into mRNA and which usually has
25 a length of 0.5 to 5 kb. Such expression control regions usually contain enhancer regions and promoter regions to which transcription factors or repressors can bind.

Expression control regions can be regulated via binding of activating or repressing factors.

5 An expression control region according to the invention contains at least the nucleic acid fragment (oligonucleotide) bp - 224 to -197 from SEQ ID NO:1 or active regulatory parts thereof. Such an oligonucleotide contains two highly conserved binding sites, region X (bp -197 to -207) and region Y (bp -224 to -214, TCF-Box). These regulatory nucleic acid fragments (regulatory regions) are also suitable as an expression control region according to the invention in combination with other promoters such as for example the TK promoter, the minimal early SV40 or the CMV immediate early promoter in expression vectors.

10 A regulatory region is understood as a region which influences expression in a negative or positive manner. If the expression control sequence according to the invention contains a negative regulatory region, the tumour-specific expression is achieved by abolishing such an inhibition in tumour cells and vice versa. The tumour-specific expression can similarly be inhibited by elements that bind to a positive regulatory region (antisense).

For a tumour-specific expression it is important that the distance between the regulatory nucleic acid fragments region X and region Y is not very large. The distance is preferably between 0 and 20 bps.

20 The human MIA region described in SEQ ID NO:1 as well as corresponding (homologous) MIA regions from mammals such as for example the mouse or rat are suitable as an expression control region. The human MIA sequence is described in the EMBL data base under the number X84707, the murine sequence under the number 485612.

25 A therapeutically active translation product is understood as a polypeptide (protein) which immediately causes a regression or ablation of tumour cells or results in this via stimulation of the immune system. Suitable genes code for example for tumour suppressor proteins, for proteins which induce apoptosis (e.g. p53), pro-drug activators (suicide genes, such as TK or cytosine deaminase (CDA)), immunostimulators (e.g. cytokines), co-stimulators (e.g. B7-1 or B7-2), CD40 and/or CD40 ligand, or toxic proteins such as cholera toxin.

5 A therapeutically active transcription product is preferably understood as an antisense sequence (e.g. ribozyme or antisense RNA) which is directed against an oncogene, a gene inhibiting apoptosis or another tumour gene such as MIA (WO 95/03328). Such a transcription product is therapeutically active because it causes a regression or ablation of tumour cells. This can for example be achieved by inhibition of the expression of a tumour gene or of an oncogene.

10 Hence such therapeutically active transcription or translation products differ from so-called indicator genes like the CAT or luciferase gene which are derived from prokaryotes or insects and are not expressed in a therapeutically active manner in mammals and only serve as an expression test.

15 Surprisingly, the expression vectors and regulatory regions according to the invention are tumour-specific or tumour-cell-specific and are in particular specific for metastatic cells since the MIA promoter is particularly active in those tumour cells which have become detached from the primary tumour and have thus become mobile.

20 The therapeutically active transcription product which is preferably an antisense nucleic acid binds in vitro under stringent conditions to a nucleic acid of the sequence SEQ ID NO:1. Such stringent standard conditions and methods for hybridization are known to a person skilled in the art and described for example by Sambrook J., et al. in "Expression of clones genes in E. coli" in Molecular Cloning: A laboratory manual (1989), Cold Spring Harbor Laboratory Press, New York, USA and Hames, B.D., and Higgins, S.J., in Nucleic Acid Hybridisation - A Practical Approach, Hames and Higgins publishers (1985), IRL Press. The standard protocols described in this manual are usually used for this. Particular reference is made to Sambrook, Section IX.

30 Preferred stringent conditions are present when hybridizing in the presence of 1 mol/l NaCl, 1 % SDS and 10 % dextran sulfate and subsequently washing the filter twice for 5 minutes at room temperature in 2 x SSC and carrying out one wash step for 30 minutes. This further wash step can be carried out at 65°C at 0.5 x SSC, 0.1 % SDS, preferably at 0.2 x SSC and 0.1 % SDS and especially preferably at 0.1 x
35 SSC, 0.1 % SDS.

5 A further subject matter of the invention is a process for the production of a tumour-specific expression vector according to the invention wherein a gene is inserted into a suitable vector in such a way that it is expressed under the control of the described expression control and/or regulatory region according to the invention. Such vectors are expediently vectors which are suitable for gene therapy. Such vectors can be either naked or formulated plasmid DNA (e.g. formulated with transfer reagents such as liposomes) or viral nucleic acids or can be artificial chromosomes.

10 The tumour-cell-specific expression vectors produced according to the invention can be advantageously used ex vivo or in vivo for gene therapy to regress or ablate tumours and tumour cells such as, e.g., melanoma, colon carcinoma and/or mamma carcinoma cells and metastasising cells derived therefrom. The regression or ablation of tumour cells can take place immediately (for example by expression of p53) or indirectly (by expression of immunostimulating agents such as cytokines
15 (e.g. IL-2, GM-CSF or IL-12) or costimulatory molecules (e.g. B7-1, B7-2, CD40).

20 A further subject matter of the invention is a process for the production of a pharmaceutical agent for the regression or ablation of primary tumours, residual tumours, metastases and minimal residual disease in vivo or ex vivo of tumour or leukaemia cells which contains an expression vector according to the invention as an essential component, and still another subject matter of the invention is the said pharmaceutical agent itself.

25 A further subject matter of the invention is a nucleic acid fragment with a length of 10 to 28 bases from the region bp -224 to -197 from SEQ ID NO:1 or a complementary nucleic acid hybridizing under stringent conditions with said fragment. Especially preferred are fragments consisting of bp -207 to -197 or -224 to 214. Such a nucleic acid fragment is suitable as a tumour cell-specific regulatory
30 element in an expression control sequence. Such a nucleic acid fragment is also suitable for the detection and identification of substances binding to this nucleic acid fragment. Such detection methods are described for example in the US patent No. 5,578,444, US patent No. 5,716,760 and the Canadian patent No. 2,112,130. In these methods the nucleic acid fragment is covalently bound to the DNA and a
35 binding partner of the nucleic acid fragment influences the DNA protein binding.

5 A further subject matter of the invention is based on the binding of elements that can bind in a complementary manner to the nucleic acid fragment (bp -197 to -224) (preferably under physiological conditions e.g. in tumour cells) in order to inhibit the expression of the MIA promoter. Such elements are for example antisense RNA, ribozyme, PNA or chimeraplasts and can be used in a modified form in the same sense as described above and/or used directly (without requiring an expression vector as a vehicle).

10 Consequently a further subject matter of the invention is a first nucleic acid fragment which specifically binds under physiological conditions to a second nucleic acid fragment of sequence SEQ ID NO:1 or a fragment thereof which comprises at least the bases from bp -224 to -197 from SEQ ID NO:1 and forms a triple helix with the double-stranded second nucleic acid fragment in the region of the bases bp -224 to -197 from SEQ ID NO:1 or contains one or several point
15 mutations in the region of the bases bp -224 to -197 from SEQ ID NO:1. Such a first nucleic acid fragment is preferably 10 to 40 nucleotides long and can be used to inhibit MIA expression in tumour cells.

20 The nucleic acid fragment (preferably factor X) represents a conserved expression control element. The mutation of a few bases (preferably 1 to 3 bases) inhibits or reduces the expression activation of the promoter element located downstream. Therefore for a therapeutic application it is preferable to introduce antisense RNA, ribozyme, PNA or chimeraplasts into tumour cells which cause such an inhibition or mutation in the MIA promoter and consequently inhibit MIA expression in
25 such cells and as a result reduce or abolish the metastasising potential of these tumour cells (preferably melanoma, mamma carcinoma, colon carcinoma).

30 According to the invention a chimeraplast is understood as a chimeric DNA-RNA hybrid molecule (expediently 60 to 90 bp) which is able to bind sequence-specifically to DNA and induce the point mutations described above. Such chimeraplasts and the production thereof are described in the US patent No. 5,565,350. Their in vivo application is described by Kren, B.T., et al., Nature Medicine 4 (1998) 285-290.

35 An expression vector according to the invention can also be used advantageously for an ex vivo purging of leukaemia cells or tumour cells in autologous bone marrow transplantations. Since the expression vector is active specifically in

tumour cells, this would enable otherwise non-detectable tumour cells to be labelled in autologous transplantation preparations. It is expedient to carry this out by using a suitable tumour cell marker as described for example in WO 95/06723. It is particularly advantageous to use the LNGFR gene as a marker gene for tumour cells from autologous bone marrow transplantation preparations. Additionally an expression vector according to the invention is used which in this case does not code for a therapeutically active product but rather for a selectable indicator gene. The preferred LNGFR gene expresses the LNGF receptor which labels the cell surface and is reliably detected by means of antibodies. This enables the undesired tumour cells to be removed from autologous bone marrow preparations. Analogously suicide genes, toxin genes and apoptosis-inducing genes can also be introduced and used to kill the tumour or leukaemia cells for purging.

The invention whose protective scope results from the claims is further elucidated by the following examples, publications, the sequence protocol and the figures. The described procedures are understood as examples which still describe the subject matter of the invention even after modifications.

Description of the Figures

- Fig. 1 Restriction map of the plasmid pCMVh12-bgh-cat.
Fig. 2 Restriction map of the plasmid pLT1.
Fig. 3 Restriction map of the plasmid pCMVhi12ireshb7-1.

Example 1

Construction of the expression vectors

1.1 Cat reporter gene as control:

Based on the reporter gene plasmid pCMVh12-bgh-cat (Fig. 1) the construct pMIA380h12-bgh-cat is prepared as follows: The CMV promoter is removed from pCMVh12-bgh-cat by a PstI/XhoI double digestion. The shortened MIA promoter fragment (0 to -380 bp) is amplified from pBL-MIA1386 (which contains the entire MIA promoter region described in Bosserhoff, A.K., et al., J. Biol. Chem. 271 (1996) 490-495) by means of PCR using appropriate primers which carry overhanging ends with the PstI/XhoI sites and cloned into the PstI/XhoI cleavage site.

1.2 Prodrug-activatable suicide gene HSV-TK:

5 Based on the construct pMIA380h12-bgh-cat the construct pMIA380h12-bgh-HSV-TK is prepared as follows: The cat gene is removed from pMIA380h12-bgh-cat by a NotI digestion. The HSV-TK gene is amplified from pLT1 (Fig. 2) by means of PCR and primers against the 5' and the 3' end of the gene, which carry overhanging ends with the NotI site and is cloned into the NotI cleavage site.

10 1.3. Immunostimulatory IL-2 gene:

Based on the construct pMIA380h12-bgh-cat the construct pMIA380h12-bgh-hIL-2 is prepared as follows: The cat gene is removed from pMIA380h12-bgh-cat by a NotI digestion. The human IL-2 gene is amplified from pCMVhIL2IREShB7-1 (Fig. 3) by means of PCR and primers against the 5' and the 3' end of the cDNA, which carry overhanging ends with the NotI sites and is cloned into the NotI cleavage site.

20 1.4 Immunostimulatory GM-CSF gene:

Based on the construct pMIA380h12-bgh-cat the construct pMIA380h12-bgh-GM-CSF is prepared as follows: The cat gene is removed from pMIA380h12-bgh-cat by a NotI digestion. GM-CSF is described in EP-B 0 202 300 and EP-B 0 188 479 (see also (Dranoff, G., et al., Proc. Natl. Acad. Sci. USA 90 (1993) 3539-3543). The GM-CSF gene is amplified by means of PCR and primers against the 5' and the 3' end of the cDNA, which carry overhanging ends with the NotI sites and is cloned into the NotI cleavage site.

Example 2

30 Transfection of the aforementioned vectors into a murine B16 melanoma cell line

The murine B16 melanoma cell line (ATCC# CRL 6322) is cultured in DMEM + 10 % FCS and L-glutamine. DOSPER (Roche Diagnostics GmbH, Mannheim, DE) is used as the transfection reagent according to the manufacturer's instructions; serum free transfection medium.

pCMVh12-bgh-cat or pMIA380h12-bgh-cat:

5 The B16 cells are transfected; the cat activity is measured after 2 to 3 days. The test for cat activity is carried out with a cat ELISA (Roche Diagnostics GmbH, Mannheim, DE) according to the manufacturer's instructions and the results obtained for the shortened MIA promoter fragment (example 1.1) are compared with those of the CMV promoter.

pCMVh12-bgh-IL-2 or pMIA380h12-bgh-IL-2:

10 The B16 cells are transfected; the IL-2 activity is measured after 2 to 3 days. The test for IL-2 activity is carried out with an IL-2 ELISA (Roche Diagnostics GmbH, Mannheim, DE) according to the manufacturer's instructions and the results obtained for the shortened MIA promoter fragment (example 1.1) are compared with those of the CMV promoter.

15 pCMVh12-bgh-HSV-TK or pMIA380h12-bgh-HSV-TK:

20 The transfection into the B16 cells is carried out with an Asp700I linearized plasmid. The plasmid pCDNA3 (Invitrogen) which contains a NeoR expression cassette is co-transfected in a 10-fold molar deficit. It is selected for 2 - 3 weeks with 50 µg/ml G418. Subsequently HSV-TK gene-positive B16 melanoma cell clones are isolated by limited dilution and PCR screening of the individual clones obtained.

25 The in vitro test for HSV-TK activity is carried out with Ganciclovir (Cymeven[®], Syntex/10 µg/ml; Beck, C., et al., Human Gene Therapy 6 (1995) 1525-1530); HSV-TK expressing positive cells die. The results obtained for the shortened MIA promoter fragment (example 1.1) are compared with those for the CMV promoter. A stable B16 melanoma cell line is set up for pMIA380h12-bgh-GM-CSF analogously to the HSV TK gene; positive clones are characterized by PCR and a GM-CSF ELISA (endogenous).

30 Example 3

Injection of the stable pMIA380h12-bgh-HSV-TK and pMIA380h12-bgh-GM-CSF transfected B16 melanoma line in syngenic C57B16 mice

35 HSV-TK:

1 x 10⁶ B16/HSV-TK cells are washed in PBS and injected subcutaneously in a volume of 200 µl into the abdominal wall of C57B16 mice (Fidler, I.), Cancer

Research 35 (1975) 218-224). The stably transfected tumour has started to grow after 4 - 6 days.

5 Variant: 1×10^5 B16/HSV-TK cells are washed in PBS and injected intravenously into the C57B16 mice. After 10 - 14 days the lung metastases have started to grow.

10 The B16 melanomas expressing HSV-TK but not the non-expressing B16 melanomas are killed by GCV doses (2 x daily; for 5 days; 150 mg/kg GCV in 200 μ l 0.9 % NaCl solution (Beck, C., et al., Human Gene Therapy 6 (1995) 1525-1530) or only 0.9 % NaCl solution as a control). The mice are sacrificed, dissected and examined histologically; the GCV-treated animals are compared with the non-treated animals.

GM-CSF(3):

15 The syngenic C57B16 mice are vaccinated by subcutaneous injection of 5×10^5 live pMIA380h12-bgh-GM-CSF transfected B16 cells into the abdomen. After 7 - 14 days the animals are challenged by subcutaneously injecting 5×10^5 live, non-transduced B16 melanoma cells into the back. The mice are sacrificed, dissected and examined when tumours of 2 - 3 cm in size occur or after at most 100 days.
20 The mice which have received an injection of B16 cells stably transfected with the GM-CSF gene under MIA promoter control are compared with mice that have received untransfected B16 cells.

Example 4

25 Injection of the plasmids pMIA380h12-bgh-HSV-TK and pMIA380h12-bgh-GM-CSF as a formulation with DOTAP (Roche Diagnostics GmbH, DE) into established B16 melanoma tumours or into normal muscle tissue of syngenic C57B16 mice

30 HSV-TK:

1×10^6 B16 cells are washed in PBS and injected subcutaneously in a volume of 200 μ l into the abdominal wall of syngenic C57B16 mice. The tumour has started to grow after 4 - 6 days. pMIA380h12-bgh-HSV-TK is formulated with DOTAP and injected into the pre-formed B16 melanoma tumours or into healthy muscle tissue.
35 Ganciclovir is administered after 2 - 3 days (2 x daily; for 5 days; 150 mg/kg GCV in 200 μ l 0.9 % NaCl solution or only 0.9 % NaCl solution as a control); the tumour cells transfected by the HSV-TK gene and therefore expressing HSV-TK are killed

by the prodrug activation but not the non-expressing cells (normal body cells or normal body cells which have been transduced by pMIA380h12-bgh-HSV-TK in which the MIA promoter is, however, not activated i.e. HSV-TK is also not expressed). The mice are sacrificed, dissected and examined; the GCV-treated animals are compared histologically with non-treated animals. The treated tissue is also compared by means of PCR and RT-PCR for the presence or expression of the transgenic HSV-TK gene.

GM-CSF:

1 x 10⁶ B16 cells are washed in PBS and injected subcutaneously in a volume of 200 µl into the abdominal wall of syngenic C57B16 mice. The tumour has started to grow after 4 - 6 days. pMIA380h12-bgh-GM-CSF is formulated with DOTAP and injected into the pre-formed B16 melanoma tumours or into muscle tissue. After 7 - 14 days the mice are sacrificed, dissected and histologically examined for the immunostimulatory effect of the GM-CSF gene (tumour size, macrophage infiltration) and for the presence of the plasmid DNA by means of PCR or for GM-CSF expression by means of RT-PCR. The mice which have received pMIA380h12-bgh-GM-CSF/ DOTAP into the pre-formed B16 melanoma tumours are compared with mice which have received only the empty vector plasmid or an injection into muscle tissue.

Example 5

Influence of mutations in the region X on MIA expression

Mutations are introduced by site-directed mutagenesis (site directed mutagenesis kit, Clontech) in region X of the expression control sequence according to Table 1 in a reporter plasmid which contains the luciferase gene under the control of the MIA promoter fragment according to SEQ ID NO:1 and expression in malignant melanoma cells (MM, B16) and non-melanoma cells (nonMM, HeLa) is examined. The result is shown in Table 1.

The reporter plasmid is prepared by inserting the MIA promoter fragment as well as the luciferase indicator gene via HindIII/BglII into the vector pGL3 basic (Promega GmbH, Mannheim, DE).

Table 1
Influence of mutations in region X on the MIA expression

| Codons from region X | MM | non-MM |
|-----------------------|-----|--------|
| TAG GCA TTT TCT | +++ | - |
| mut 1 --X -XX XXX --- | - | - |
| mut 3 --- X-X --- --- | - | - |
| mut 4 --X X-X --- --- | - | - |
| mut 5 --X --- --- --- | ++ | - |
| mut 6 --- --X --- --- | + | - |

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Patent Claims

1. Tumour cell-specific expression vector containing a gene which codes for a transcription or translation product that is therapeutically active in tumour cells, wherein this gene is under the control of an expression control region with the sequence SEQ ID NO:1 or a fragment thereof which comprises at least the bases bp -224 to -214 and/or -197 to -207 from SEQ ID NO:1.
2. Expression vector as claimed in claim 1, wherein the therapeutically active transcription or translation product causes tumour regression, tumour ablation or immunostimulation in tumour cells.
3. Expression vector as claimed in claim 1, wherein the therapeutically active transcription product is an antisense nucleic acid or a ribozyme which binds in vitro under stringent conditions to a nucleic acid of sequence SEQ ID NO:1.
4. Expression vector as claimed in claim 1 or 2, wherein the therapeutically active translation product is a prodrug-activating, an apoptosis-inducing, tumour-suppressing, immunostimulating, co-stimulatory or toxic polypeptide.
5. Process for the production of a tumour-specific expression vector as claimed in claims 1 to 4, wherein the therapeutically active gene is inserted in such a way that it is expressed under the control of the expression control region.
6. Use of an expression vector as claimed in claims 1 to 4 for the regression or ablation of primary tumours, residual tumours, metastases and minimal residual disease in vivo or ex vivo of tumour and leukaemia cells.
7. Process for the production of a pharmaceutical agent for the regression or ablation of primary tumours, residual tumours, metastases and minimal residual disease in vivo or ex vivo of tumour and leukaemia cells, wherein an expression vector as claimed in claims 1 to 4 is used as an essential component of the agent.

8. Pharmaceutical agent for the regression or ablation of primary tumours, residual tumours, metastases and minimal residual disease in vivo or ex vivo of tumour and leukaemia cells, wherein it contains an expression vector as claimed in claims 1 to 4 as an essential component.
- 5 9. Nucleic acid fragment with a length of 10 to 30 bases, wherein the fragment hybridizes under stringent conditions with the base sequence -224 to -197 from SEQ ID NO:1 or with a nucleic acid which is complementary thereto.
- 10 10. Use of a nucleic acid fragment of sequence SEQ ID NO:1 or a fragment thereof which comprises at least the bases bp -224 to -197 from SEQ ID NO:1 in a method for the detection of a DNA-protein binding, wherein the nucleic acid fragment is covalently bound to the DNA and a binding partner of the nucleic acid fragment influences the DNA-protein binding.
- 15 11. Nucleic acid fragment which specifically binds under physiological conditions to a second nucleic acid fragment of sequence SEQ ID NO:1 or a fragment thereof which comprises at least the bases bp -224 to -197 from SEQ ID NO:1 and forms a triple helix with the double-stranded second nucleic acid fragment in the region of the bases bp -224 to -197 from SEQ ID NO:1 or contains one or several point mutations in the region of the bases bp -224 to -197 from SEQ ID NO:1.
- 20 12. Use of a first nucleic acid fragment as claimed in claim 11 for the inhibition of the MIA expression in tumour cells.

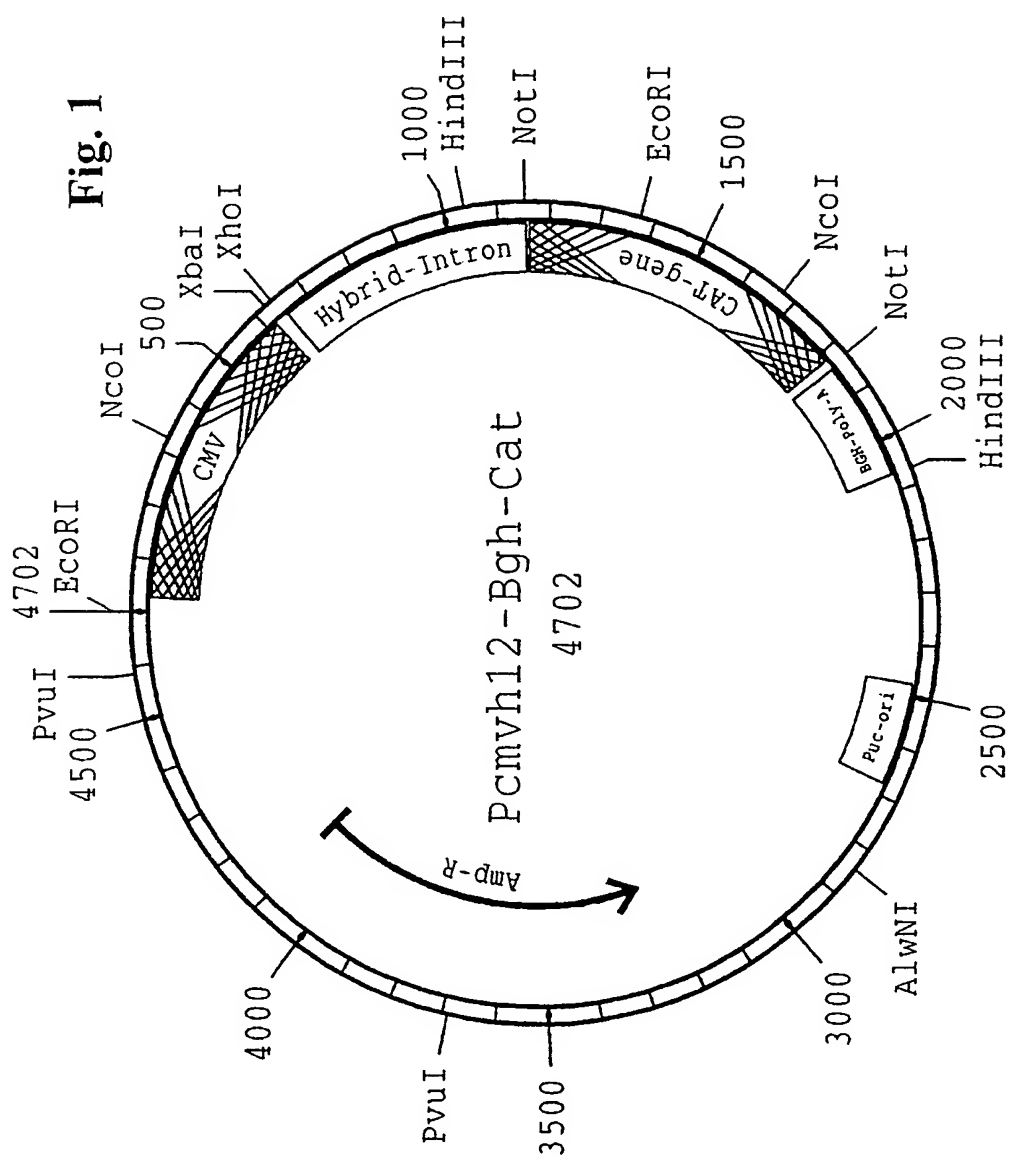


Fig. 2

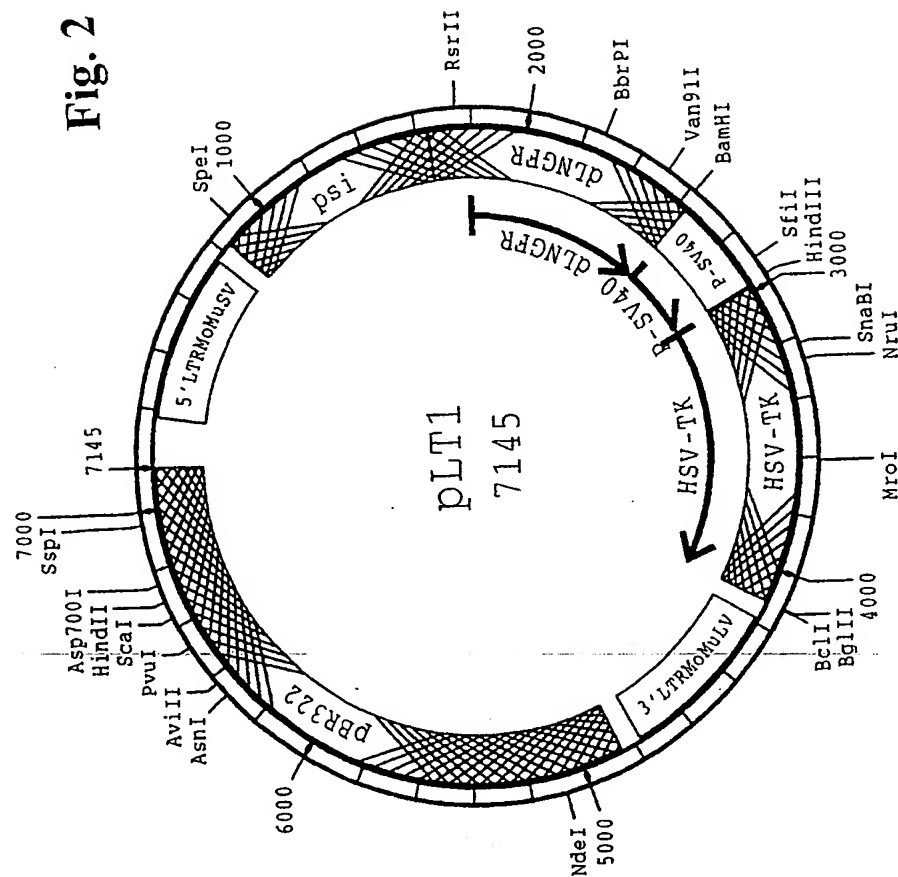
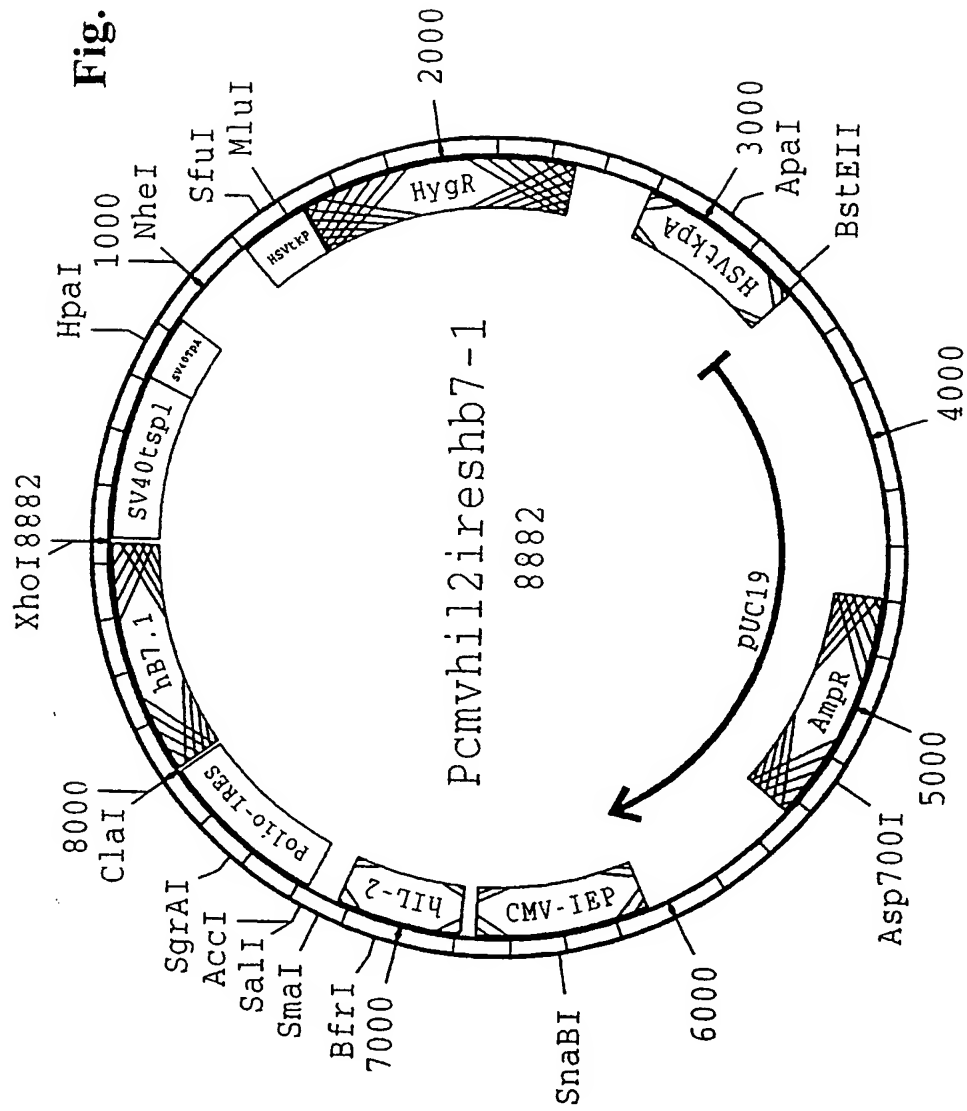


Fig. 3



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT:
(A) NAME: ROCHE DIAGNOSTICS GMBH
(B) STREET: Sandhofer Str. 116
(C) CITY: Mannheim
10 (E) COUNTRY: Germany
(F) POSTAL CODE (ZIP): D-68305
(G) TELEPHONE: 08856/60-3446
(H) TELEFAX: 08856/60-3451
- 15 (ii) TITLE OF INVENTION: Tumour-specific expression control
region and the use thereof
- (iii) NUMBER OF SEQUENCES: 1
- 20 (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B
(EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "expression control region
Base 1 = -380 Base 380 = -1"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTTTACAGGC TCCTCCGCTT CTGTGGCCAG AGGGGACAGC GGAGGACCCC AGGTACCTAA 60
45 GCCAACTCAA GAGAAGATGG AATTGAATAT TTCAACCACC TTATCTAGGC CTCTGTGATT 120
GTTGAGGAGG GGGCTGTCAC TGGGAAAGTT GTGAGCTGCT TTGGACCTTA TCTGGGAATT 180
TCCTTGGGCC TTACAGCTTT ACCCTATCCT TGAAATGGTT CTGGTTTCAT AGCAACTTCT 240
50 AGGTGGTGTG GGCGAAGTTT GGGACTGGTT TAGGGCGGGG ACAAGACCAA GAACACAAGT 300
TTCCTTGATC GGGAGAGAGG GAGGGGAGGA AATTGGAGAC CCCAGACCCC CCTTGCTCAC 360
55 TCTCTTGCTC ACAGTCCACG ATG 383

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 99/02031

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| A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/12 C07K14/47 C12N15/85 A61K48/00 | | |
| According to International Patent Classification (IPC) or to both national classification and IPC | | |
| B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K C12N | | |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched | | |
| Electronic data base consulted during the international search (name of data base and, where practical, search terms used) | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category: | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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| <input checked="" type="checkbox"/> | Further documents are listed in the continuation of box C. | |
| <input checked="" type="checkbox"/> | Patent family members are listed in annex | |
| * Special categories of cited documents: | | |
| "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed | | |
| "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family | | |
| Date of the actual completion of the international search 13 January 2000 | | Date of mailing of the international search report 19/01/2000 |
| Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel: (+31-70) 340-2040, Tx. 31 651 epo nl. Fax: (+31-70) 340-3016 | | Authorized officer De Kok, A |

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